```
1 CCATGGGAGC GAACACTTCA AGAAAACCAC CAGTGTTTGA TGAAAATGAA
   51 GATGTCAACT TTGACCACTT TGAAATTTTG CGAGCCATTG GGAAAGGCAG
 101 TTTTGGGGAG GTCTGCATTG TACAGAAGAA TGATACCAAG AAGATGTGCG
 151 CAATGAAGTA CATGAATAAA CAAAAGTGCG TGGAGCGCAA TGAAGTGAGA
 201 AATGTCTTCA AGGAACTCCA GATCATGCAG GGTCTGGAGC ACCCTTTCCT
 251 GGTTAATITG TGGTATTCCT TCCAAGATGA GGAAGACATG TTCATGGTGG
 301 TGGACCTCCT GCTGGGTGGA GACCTGCGTT ATCACCTGCA ACAGAACGTC
 351 CACTTCAAGG AAGAAACAGT GAAGCTCTTC ATCTGTGAGC TGGTCATGGC 401 CCTGGACTAC CTGCAGAACC AGCGCATCAT TCACAGGGAT ATGAAGCCTG 451 ACAATATTT ACTTGACGAA CATGGGCACG TGCACATCAC AGATTTCAAC
  501 ATTGCTGCGA TGCTGCCCAG GGAGACACAG ATTACCACCA TGGCTGGCAC
  551 CAAGCCTTAC ATGGCACCTG AGATGTTCAG CTCCAGAAAA GGAGCAGGCT
  601 ATTCCTTTGC TGTTGACTGG TGGTCCCTGG GAGTGACGGC ATATGAACTG
651 CTGAGAGGCC GGAGACCGTA TCATATTCGC TCCAGTACTT CCAGCAAGGA
  701 AATTGTACAC ACGTTTGAGA CGACTGTTGT AACTTACCCT TCTGCCTGGT 751 CACAGGAAAT GGTGTCACTT CTTAAAAAGC TACTCGAACC TAATCCAGAC
  801 CAACGATTIT CTCAGTTATC TGATGTCCAG AACTTCCCGT ATATGAATGA
  851 TATAAACTGG GATGCAGTTT TTCAGAAGAG GCTCATTCCA GGTTTCATTC
901 CTAATAAAGG CAGGCTGAAT TGTGATCCTA CCTTTGAACT TGAGGAAATG
951 ATTTTGGAGT CCAAACCTCT ACATAAGAAA AAAAAGCGTC TGGCAAAGAA
1001 GGAGAAGGAT ATGAGGAAAT GCGATTCTTC TCAGACATGT CTTCTTCAAG
 1051 AGCACCTTGA CTCTGTCCAG AAGGAGTTCA TAATTTTCAA CAGAGAAAAA
 1101 GTAAACAGGG ACTITAACAA AAGACAACCA AATCTAGCCT TGGAACAAAC
 1151 CAAAGACCCA CAAGGTGAGG ATGGTCAGAA TAACAACTTG TAAAGGCCTC
 1201 ATGTCTTCTT CTTGGGACAA TCTCATGCCA GAAACTTCTA ATTACATATG
1251 TCAAGAAAAG CTGACAGTAG CTCCTGCCAC TCCACACAC ATGACTTAGA
1301 AAATGTGAAT GAATATATTT CAAAAAAAGGC AGCACAACAC AGTGAAGGGT
1351 CCTGGGCCTG AGCTCCTGGA AAGTCATTC ACATCAATCA ACTGTGTGAT
 (SED NO:1)
5'UTR:
Start Codon: 3
Stop Codon:
                       1191
3'UTR:
                       1194
Homologous proteins:
Top 10 BLAST Hits
                                                                                                             score
CRA | 8700000001426 /altid=gi | 7161864 /def=emb | CAB76566.1 | (AJ25... CRA | 87000000001314 /altid=gi | 8923754 /def=ref | NP_060871.1 | gene... CRA | 103000001515936 /altid=gi | 10946600 /def=ref | NP_067277.1 | hy... CRA | 108000024647823 /altid=gi | 12730486 /def=ref | XP_003392.2 | ge... CRA | 18000005184360 /altid=gi | 7505957 /def=pir | | T23688 hypotheti... CRA | 18000005004115 /altid=gi | 1730069 /def=sp| P54644 | KRAC_DICDI ... CRA | 18000004912236 /altid=gi | 464395 /def=sp| P28178 | PK2_DICDI PR... CRA | 18000004991065 /altid=gi | 1362152 /def=pir | | S56639 ribosomal ... CRA | 18000004952305 /altid=gi | 462434 /def=sp| P34099 | KAPC_DICDI C... CRA | 107000045076305 /altid=gi | 12322721 /def=gb | AAG51345.1 | AC012 ...
                                                                                                                        e-158
                                                                                                                560
                                                                                                                 557.
                                                                                                                        e-157
                                                                                                                 514
                                                                                                                        e-145
                                                                                                                 395
                                                                                                                         e-109
                                                                                                                 328
                                                                                                                        8e-89
                                                                                                                 226
                                                                                                                         5e-58
                                                                                                                 209
                                                                                                                         8e-53
                                                                                                                 204
                                                                                                                         3e-51
                                                                                                                         6e-51
                                                                                                                 203
                                                                                                                 202
                                                                                                                         8e-51
 EST:
                                                                                                  Score
                                                                                                                1362
                                                                                                                         0.0
 gi|12432521 /dataset=dbest /taxon=96...
gi|12425892 /dataset=dbest /taxon=96...
gi|9811536 /dataset=dbest /taxon=960...
                                                                                                                  864
                                                                                                                         0.0
                                                                                                                 708
                                                                                                                         0.0
  EXPRESSION INFORMATION FOR MODULATORY USE:
 gi|12432521 brain hippocampus
gi|12425892 Breast mammary adenocarcinoma cell line
 gi|9811536 Bladder carcinoma cell line
  <u>Tissue expression:</u>
  Human brain
  Human fetal brain
  Human fetal heart
  Human kidney
  Human uterus
```

```
1 MGANTSRKPP VFDENEDVNF DHFEILRAIG KGSFGEVCIV QKNDTKKMCA 51 MKYMNKQKCV ERNEVRNYFK ELQIMQGLEH PFLVNLWYSF QDEEDMFMVV 101 DLLLGGDLRY HLQQNVHFKE ETVKLFICEL VMALDYLQNQ RIIHRDMKPD 151 NILLDEHGHV HITDFNIAAM LPRETQITTM AGTKPYMAPE MFSSRKGAGY 201 SFAVDWWSLG VTAYELLRGR RPYHIRSSTS SKEIVHTFET TVVTYPSAWS 251 QEMVSLLKKL LEPNPDQRFS QLSDVQNFPY MNDINWDAVF QKRLIPGFIP 301 NKGRLNCDPT FELEEMILES KPLHKKKKRL AKKEKDMRKC DSSQTCLLQE 351 HLDSVQKEFI IFNREKVNRD FNKRQPNLAL EQTKDPQGED GQNNNL (SEQ ID NO:2)
     (SEQ ID NO:2)
FEATURES:
Functional domains and key regions:
[1] PDOCO0001 PS00001 ASN_GLYCOSYLATION
N-glycosylation site
Number of matches: 2
1 4-7 NTSR
2 43-46 NDTK
 [2] PDOC00005 PS00005 PKC_PHOSPHO_SITE
Protein kinase C phosphorylation site
Number of matches: 7
1 5-7 TSR
2 6-8 SRK
3 194-196 SRK
4 45-47 TKK
5 122-124 TVK
                     193-195 SSR
                             6-8 SRK
 [3] PDOC00006 PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site
 Number of matches: 4

1 33-36 SFGE

2 89-92 SFQD

3 212-215 TAYE
                      230-233 SSKE
  [4] PDOC00008 PS00008 MYRISTYL
  N-myristoylation site
  Number of matches: 3
1 2-7 GANTSR
2 197-202 GAGYSF
                      391-396 GQNNNL
  [5] PDOC00009 PS00009 AMIDATION
  Amidation site
                      218-221 RGRR
   [6] PDOC00100 PS00107 PROTEIN_KINASE_ATP
   Protein kinases ATP-binding region signature
                          29-52 IGKGSFGEVCIVQKNDTKKMCAMK
   [7] PDOC00100 PS00108 PROTEIN_KINASE_ST
   Serine/Threonine protein kinases active-site signature
                       142-154 IIHRDMKPDNILL
   Membrane spanning structure and domains:
Helix Begin End Score Certainity
                                End
217
                                            0.690 Putative
```

```
BLAST Alignment t T p Hit:
Alignment to top blast hit:
>CRA|87000000001426 /altid=gi|7161864 /def=emb|CAB76566.1| (AJ250840)

serine/threonine protein kinase [Mus musculus] /org=Mus
musculus /taxon=10090 /dataset=nraa /length=414
              Length = 414
 Score = 560 bits (1428), Expect = e-158 Identities = 278/403 (68%), Positives = 320/403 (78%), Gaps = 7/403 (1%)
                MGANTSRKPPVFDENEDVNFDHFEILRAIGKGSFGEVCIVQKNDTKKMCAMKYMNKQKCV 182
                MG N S KPPVFDENE+VNFDHF+ILRAIGKGSFG+VCIVQK DTKKM AMKYMNKQKCV
Query: 3
                 MGGNHSHKPPVFDENEEVNFDHFQILRAIGKGSFGKVCIVQKRDTKKMYAMKYMNKQKCV 60
Sbjct: 1
                 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVHFKE 362
                 ER+EVRNVF+ELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVHF E
 Query: 183
                 ERDEVRNVFRELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVHFTE 120
 Sbjct: 61
                 ETVKLFICELVMALDYLQNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 542
 Query: 363
                                             IIHRD+KPDNILLDEHGHVHITDFNIA +L
                   TVKL+ICEL +AL+YLQ
                 GTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFNIATVLKGSEKASSM 180
 Sbjct: 121
                 AGTKPYMAPEMFS--SRKGAGYSFAVDWWSLGVTAYELLRGRRPYHIRSSTSSKEIVHTF 716
 Query: 543
                                          G GYS+ VDWWSLGVTAYELLRG RPY I S+T
                 AGTKPYMAPEVFQVYVDGGPGYSYPVDWWSLGVTAYELLRGWRPYEIHSATPIDEILNMF 240
                  AGTKPYMAPE+F
 Sbjct: 181
                 ETTVVTYPSAWSQEMVSLLKKLLEPNPDQRFSQLSDVQNFPYMNDINWDAVFQKRLIPGF 896
                 + VYSW+ MVSLLKKLL +P+RSLD+Q+Y+D+NWDAVF+KL+PGF
KVERVHYSSTWCEGMVSLLKKLLTKDPESRLSSLRDIQSMTYLADMNWDAVFEKALMPGF300
 Query: 717
 Sbjct: 241
                 IPNKGRLNCDPTFELEEMILESKPLHKKKKRLAK-KEKDMRKCDSSQTCLLQEHLDSVQK 1073
 Query: 897
                 +PNKGRLNCDPTFELEEMILESKPLHKKKKRLAK + +D K LQ+ L++V+K

+PNKGRLNCDPTFELEEMILESKPLHKKKKRLAKHRSRDSTKDSCPLNGHLQQCLETVRK 360
 Sbjct: 301
 Query: 1074 EFIIFNREKVNR----DFNKRQPNLALEQTKDPQGEDGQNNNL 1190 EFIIFNREK+ R D + + + +DG+NNN+
  EFIIFNREK+ R D + + + +DG+NNN+
Sbjct: 361 EFIIFNREKLRRQQGHDGQLSDLDGRIGSQTSSKLQDGRNNNI 403 (SEQ ID NO:4)
  >CRA|8700000001314 /altid=gi|8923754 /def=ref|NP_060871.1| gene for serine/threonine protein kinase [Homo sapiens] /org=Homo sapiens /taxon=9606 /dataset=nraa /length=414
   Score = 557 bits (1419), Expect = e-157 Identities = 275/403 (68%), Positives = 319/403 (78%), Gaps = 7/403 (1%)
    Frame = +3
                   MGANTSRKPPVFDENEDVNFDHFEILRAIGKGSFGEVCIVQKNDTKKMCAMKYMNKQKCV 182
   Query: 3
                   MG N S KPPVFDENE+VNFDHF+ILRAIGKGSFG+VCIVQK DTKKM AMKYMNKQKC+
                   MGGNHSHKPPVFDENEEVNFDHFQILRAIGKGSFGKVCIVQKRDTKKMYAMKYMNKQKCI 60
   Sbjct: 1
                   ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVHFKE 362
ER+EVRNVF+ELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVHF E
ERDEVRNVFRELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVHFTE 120
   Query: 183
   Sbict: 61
                   ETVKLFICELVMALDYLQNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 542
TVKL+ICEL +AL+YLQ IIHRD+KPDNILLDEHGHVHITDFNIA ++ + ++M
   Query: 363
                   GTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFNIATVVKGAERASSM 180
   Sbjct: 121
                   AGTKPYMAPEMFS--SRKGAGYSFAVDWWSLGVTAYELLRGRRPYHIRSSTSSKEIVHTF 716
AGTKPYMAPEHF +G GYS+ VDWWSLG+TAYELLRG RPY I S T EI++ F
   Query: 543
                   AGTKPYMAPEVFQVYMDRGPGYSYPVDWWSLGITAYELLRGWRPYEIHSVTPIDEILNMF 240
   Sbjct: 181
                   ETTVVTYPSAWSQEMVSLLKKLLEPNPDQRFSQLSDVQNFPYMNDINWDAVFQKRLIPGF 896
                    + V Y S W + MV+LL+KLL +P+ R S L D+Q+ PY+ D+NWDAVF+K L+PGF
KVERVHYSSTWCKGMVALLRKLLTKDPESRVSSLHDIQSVPYLADMNWDAVFKKALMPGF 300
   Query: 717
    Sbjct: 241
                   IPNKGRLNCDPTFELEEMILESKPLHKKKKRLAK-KEKDMRKCDSSQTCLLQEHLDSVQK 1073 +PNKGRLNCDPTFELEEMILESKPLHKKKKRLAK + +D K LQ L++V++ VPNKGRLNCDPTFELEEMILESKPLHKKKKRLAKNRSRDGTKDSCPLNGHLQHCLETVRE 360
    Query: 897
    Sbjct: 301
    Query: 1074 EFIIFNREKVNRDFNKRQPNLALEQTKDPQG----EDGQNNNL 1190
EFIIFNREK+ R + L + Q +DG NNNL
    Sbjct: 361 EFIIFNREKLRRQQGQGSQLLDTDSRGGGQAQSKLQDGCNNNL 403 (SEQ ID NO:5)
                     EFIIFNREK+ R +
```

Score = 514 bits (1310), Expect = e-145 Identities = 250/389 (64%), Positives = 304/389 (77%), Gaps = 4/389 (1%) Frame = +3Query: 18 SRKPPVFDENEDVNFDHFEILRAIGKGSFGEVCIVQKNDTKKMCAMKYMNKQKCVERNEV 197 S + PVFD+ EDVNFDHF+ILRAIGKGSFG+VCIVQK DT+KM AMKYMNKQ+C+ER+EV Sbjct: 77 SARRPVFDDKEDVNFDHFQILRAIGKGSFGKVCIVQKRDTEKMYAMKYMNKQQCIERDEV 136 RNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVHFKEETVKL 377 RNVF+EL+I+Q +EH FLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNV F E+TV+L RNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVQFSEDTVRL 196 Query: 198 Sbjct: 137 FICELVMALDYLQNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTMAGTKP 557 +ICE+ +ALDYL++Q IIHRD+KPDNILLDE GH H+TDFNIA ++ + T +AGTKP Query: 378 Sbjct: 197 YICEMALALDYLRSQHIIHRDVKPDNILLDEQGHAHLTDFNIATIIKDGERATALAGTKP 256 Query: 558 YMAPEMFSS--RKGAGYSFAVDWWSLGVTAYELLRGRRPYHIRSSTSSKEIVHTFETTVV 731 YMAPE+F S G GYSF VDWWS+GV AYELLRG RPY I SS + + +V F T V YMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDIHSSNAVESLVQLFSTVSV 316 Sbict: 257 TYPSAWSQEMVSLLKKLLEPNPDQRFSQLSDVQNFPYMNDINWDAVFQKRLIPGFIPNKG 911 Y WS+EMV+LL+KLL NP+ RFS L D+Q P + + WD + +K++ PGF+PNKG QYVPTWSKEMVALLRKLLTVNPEHRFSSLQDMQTAPSLAHVLWDDLSEKKVEPGFVPNKG 376 Query: 732 Sbjct: 317 RLNCDPTFELEEMILESKPLHKKKKRLAKKEKDMRKCDSSQT--CLLQEHLDSVQKEFII 1085 Query: 912 RL+CDPTFELEEMILES+PLHKKKKRLAK + DSSQ+ LO+ LD++O++F+I Sbjct: 377 RLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDSSRDSSQSENDYLQDCLDAIQQDFVI 436 Query: 1086 FNREKVNRDFNKRQPNLALEQTKDPQGED 1172 FNREK+ KR L E Sbjct: 437 FNREKL----KRSQELMSEPPPGPETSD 460 (SEQ ID NO:6) Score = 395 bits (1004), Expect = e-109 Identities = 199/316 (62%), Positives = 237/316 (74%), Gaps = 7/316 (2%) Frame = +3Query: 264 YSFQDEEDMFMVVDLLLGGDLRYHLQQNVHFKEETVKLFICELVMALDYLQNQRIIHRDM 443 YSFQDEEDMFMVVDLLLGGDLRYHLQQNVHF E TVKL+ICEL +AL+YLQ IIHRD+ YSFQDEEDMFMVVDLLLGGDLRYHLQQNVHFTEGTVKLYICELALALEYLQRYHIIHRDI 63 Sbjct: 4 KPDNILLDEHGHVHITDFNIAAMLPRETQITTMAGTKPYMAPEMFS--SRKGAGYSFAVD 617 Query: 444 KPDNILLDEHGHVHITDFNIA ++ + ++MAGTKPYMAPE+F +G GYS+ VD Sbict: 64 KPDNILLDEHGHVHITDFNIATVVKGAERASSMAGTKPYMAPEVFQVYMDRGPGYSYPVD 123 Query: 618 WWSLGVTAYELLRGRRPYHIRSSTSSKEIVHTFETTVVTYPSAWSQEMVSLLKKLLEPNP 797 WWSLG+TAYELLRG RPY I S T EI++ F+ V Y S W + MV+LL+KLL +P WWSLGITAYELLRGWRPYEIHSVTPIDEILNMFKVERVHYSSTWCKGMVALLRKLLTKDP 183 Sbjct: 124 DQRFSQLSDVQNFPYMNDINWDAVFQKRLIPGFIPNKGRLNCDPTFELEEMILESKPLHK 977 Query: 798 + R S L D+Q+ PY+ D+NWDAVF+K L+PGF+PNKGRLNCDPTFELEEMILESKPLHK Sbjct: 184 ESRVSSLHDIQSVPYLADMNWDAVFKKALMPGFVPNKGRLNCDPTFELEEMILESKPLHK 243 Query: 978 KKKRLAK-KEKDMRKCDSSQTCLLQEHLDSVQKEFIIFNREKVNRDFNKRQPNLALEQTK 1154 KKKRLAK + +D K LQ L++V++EFIIFNREK+ R + L + KKKRLAKNRSRDGTKDSCPLNGHLQHCLETVREEFIIFNREKLRRQQGQGSQLLDTDSRG 303 Sbjct: 244 Query: 1155 DPQG----EDGQNNNL 1190 +DG NNNL Sbjct: 304 GGQAQSKLQDGCNNNL 319 (SEQ ID NO: 7) >CRA|18000005184360 /altid=gi|7505957 /def=pir||T23688 hypothetical protein M03C11.1 - Caenorhabditis elegans /org=Caenorhabditis elegans /taxon=6239 /dataset=nraa /length=379 Length = 379

## FIGURE 2C

```
Score = 328 bits (833), Expect = 8e-89 Identities = 156/353 (44%), Positives = 226/353 (63%), Gaps = 2/353 (0%)
  Frame = +3
                  HFEILRAIGKGSFGEVCIVQKNDTKKMCAMKYMNKQKCVERNEVRNVFKELQIMQGLEHP 245
HF ++R+IG+G+FG+VCIVQ+ TKK A+KYMNK++C+E+ NV +EL ++ + HP
HFSVIRSIGRGAFGKVCIVQERKTKKYFALKYMNKRRCIEKGVAANVIRELTLLSKMSHP 86
 Query: 66
Sbjct: 27
                  FLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVHFKEETVKLFICELVMALDYLQNQR 425
Query: 246
                   F+VNLWY+FQD + M+MV DLLLGGDLRYHL Q
                                                                         F E+ KL++CE+ +A++YL
Sbjct: 87
                  FIVNLWYTFQDGDYMYMVSDLLLGGDLRYHLSQQGKFAEDRAKLYLCEICLAVEYLHEMK 146
Query: 426
                  IIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTMAGTKPYMAPEMFSS--RKGAG 599
                  I+HRD+KP+NILLDE GH H+TD N+A L + T+ +GT+PYMAPE++++ G
IVHRDIKPENILLDEQGHAHLTDLNLATQLEDDQLATSYSGTRPYMAPEIYATYLEIEDG 206
Sbjct: 147
Query: 600
                  YSFAVDWWSLGVTAYELLRGRRPYHIRSSTSSKEIVHTFETTVVTYPSAWSQEMVSLLKK 779
                         VDWW+LGV YE+LRGR P+ S T +E
                                                                            F + + YP+ W +++
                  YDSRVDWWALGVCFYEMLRGRTPFEFSSRTKPEEAYVAFRESSIPYPAHWPTDLIQFINS 266
Sbjct: 207
Query: 780 LLEPNPDQRFSQLSDVQNFPYMNDINWDAVFQKRLIPGFIPNKGRLNCDPTFELEEMILE 959
                  +L+ + ++R L ++ Y I++ +VF+K+ P FIP K LNCDP +ELEE IL MLKFDKEKRLVGLEAIKKHSYTERIDFKSVFEKKPSPVFIPCKEGLNCDPMYELEERILV 326
Sbjct: 267
                  SKPLHKKKKRLAKKEKDMRKCDSSQTCLLQEHLDSVQKEFIIFNREKVNRDFN 1118
Query: 960
                  S P+H ++R R Q L E V K FI F+R V + N
STPIH--RRTNHNNSSGRSSSEPQNAALVE----VSKAFIDFSRHNVKIEPN 373 (SEQ ID NO: 8)
Sbjct: 327
Hmmer search results (Pfam):
Scores for sequence family classification (score includes all domains):
             Description
                                                                                       Score
                                                                                                    E-value N
PF00069 Eukaryotic protein kinase domain
CE00359 E00359 bone_morphogenetic_protein_receptor
PF00433 Protein kinase C terminal domain
CE00022 CE00022 MAGUK_subfamily_d
CE00203 CE00203 ERBB_RECEPTOR
CE00031 CE00031 VEGFR
CE00528 CE00528 CDC14_PHOSPHATASE
CE00292 CE00292 PTK_membrane_span
CE00287 CF00286 PTK_Eph_orphan_receptor
F00286 PTK_EGF_receptor
                                                                                       241.7
                                                                                                        1e-68
                                                                                                    0.00012
0.2
0.02
0.25
                                                                                        18.9
                                                                                          8.8
                                                                                          8.6
                                                                                          6.0
                                                                                          5.1
                                                                                                         0.12
                                                                                          1.7
                                                                                       -44.9
                                                                                                    1.9e-06
                                                                                       -45.1
-59.9
                                                                                                    2.4e-05
1.7e-07
CE00286 E00286 PTK_EGF_receptor
CE00291 CE00291 PTK_fgf_receptor
CE00290 CE00290 PTK_Trk_family
CE00016 CE00016 GSK_glycogen_synthase_kinase
                                                                                                    0.00049
                                                                                       -81.9
                                                                                       -158.8
                                                                                       216.0
                                                                                                     0.00011
                                                                                                                    1
 CE00288 CE00288 PTK_Insulin_receptor
```

Parsed fo Model	or domain Domain	ns: seq-f	seq-t	hmm-f	hmm-t	score	E-value
CE00031	1/1	134	168	1059	1093 891	5.1 6.0	0.12 0.25
CE00203 CE00359	1/1 1/1	136 142	172 191	855 272	326	18.9	0.00012
CE00022 CE00288	1/1 1/1	133 23	223 238	133 1	226 269 []	8.6 -225.8	0.21
CE00528 CE00292	$\frac{1}{1}$ $\frac{1}{1}$	251 23	260 276	608 1	617 .] 288 []	1.7 -44.9	1.9e-06
CE00287 CE00291	$\frac{1}{1}$	23 23		1 1	260 [] 285 []	-45.1 -81.9	2.4e-05 0.00049
CE00286	$\frac{1}{1}$	23 23	278	1 1	263 [] 282 []	-59.9 -158.8	1.7e-07 0.00022
CE00290 PF00069	1/1	23 282	281	. <u>ī</u>	278 [] 20 [.	241.7 8.8	1e-68 0.2
PF00433	1/1 1/1	202 1	331	. 1	433	-216.0	0.00011

_					
_1	TCCCTCTCTC	ATACCATTTA	ATTGGTTGCT	TCCTAATTAA	TGACTCTCTT
51	TGCTCTCTAT	TTAATGATTC	TTGCTAAAGT	CCATAAGGCA	CTTTGCCAGC
101	AGTTGGTTTT	TAGTATGAAA	<b>AGTAGCATTT</b>	CCTTAATGAG	TCTGAGTCTG
151	CCTTCCAAAT	GAAGGGTTTA	CTTACATTTT	CCTAATGGGA	AAACGAGCTT
201	TTCTTCTACG	CTTCCTTAGG	GGTTTCATAA	GTTCTTTTTC	AATAACTCAT
251	CCTTAACACT	TTCTCCAATT	CTGCCTGTAA	TCAATATTCC	CTTCACATGT
301	AAAGAGCTCA	GGAGGAAATC	AACTATITT	TTAAAAATAC	GCAATAAGGA
351	AATTCTGCTA	CTCTTAGAAA	TAGCAGGAGC	TAACATTCAT	TCTTTCCATA
401	TCATGTGCTA	GGCATTGTGC	CAATTACCTT	ATATACATTC	
451	TCTATCCATC	ACCATATATC	TOOTAACCAT	CAAATTTTCT	TCTCATTATA
201 201	ACCTCACTAC	ACCATATATG	TATTATTE	GAAATITICT	IAAGCCAGAI
201	AGCIGAGIAG	AATTTTAAAA	IAIIAIIIIG	TACAAAATCT	AGACCTTTAC
33T	CCCATTIGGG	GGATAGATCT	GAAGATCTGG	GCTCATGTTT	CCATGTGGTG
60T	ACAATCTGTT	TGATCTGAGC	ACAATTACTT	TATTTGGATG	GAGCCATTGC
651	CACCATTGTC	TGCCCAATGC	ACTAATGTTA	AATGCCCAGT	CTGGCTCACT
701	CATTTGCATC	ATCTGCCTGG	CTCCTATAGG	GATCCCAGCT	TGTCACTCCT
751	GAGGTAGACA	CTGTCATTTC	CCCCATTCTA	GAGGTGAGAG	GTTACATAAC
801	TGGGCCAAAG	<b>GCATTATCAG</b>	<b>TGTCAGTTTT</b>	AGGACTGGAA	CACAGGATGC
851	TGCCTCTCTT	TACCATTATG	TTTTAAAGTG	GAGCAAAGCC	GTAGTTTTCA
901	GGATCTTTTC	TTGTTCACAC	ATATCATTTA	ATTTGAGCCT	CAGAGCGGCT
951	AACAGTTTTG	AGCACTTATG	CTATGAAAAT	GTTTTGTGTA	TTCAGTTAAA
1001	TGTATGCATA	TCATACATTT	ATGTAACTCA	ATACATATAT	ATAAATGTGA
1051	TATAACATAC	GTATGATATA	ACAGAGTTAT	ATATATCTCT	ATTATTTAAC
1101	TTAATATATA	ATGAGTTAAG	TCTATCCATA	TCATACATTT	ATIAITIAAC
1151	ATATATAAAC	ACTTATATA	TACAACACAC	TTCATAGATTI	AIGIAACICA
1201	CTATATAAAG	AGTTATATAA	TACAACAGAG	TIGATATATA	IAIAAAIGII
1701	GIATATAAAC	ATAATATATA	CGITAATATA	TATTAACAAA	GAGIIGIAIA
152T	ATACAACACA	GAGTTAATAA	TATATAAATA	CAACACAAAG	AGTTATATAT
T30T	GIGIGIATIA	TACATTTAAC	TTAATATATA	ATGAGTTAAA	TGTATGTCTG
1351	TCCCATTCAA	CTCTCCATTG	AGGAAAGTAC	CATTATCTTC	CCCAAGTTCA
1401	GAAGAAGAAA	ACAGAGAAAT	ATATTGAAAT	TCAGCAATTT	GCTGGTGTGG
1451	TCAAGTCCAA	CCCAGAACTT	GCTTCTTTTA	CATTGTAGTA	CCCTCCAGGG
1501	TATGCAGAAA	CAGATAGCTA	GTGCATCTTT	ATGACTAAAA	AAGAAAATTT
1551	TTGTTGTTGA	TTACCCAGTA	ACAACAAGAC	AGTATAAAAT	CAGCATATTT
1601	TCTCAACAAT	ATTITCATTT	TATAGTTGTT	GAATAAAGTA	TTGCTGACTT
	CATTTTAAAC	TTTTCTACAT	ACTTTGAAAA	ATATETTECT	TTCCTCCCAT
1701	TTTGTAAGTC	TAGGTCTGCT	ATTENTENCE	CATCCACTCT	TTTCTCCCCAT
	TECTTEATET	TTTTATTCTG	AAATCATCCT	TECTTTTEAN	ACACAAAACT
	TTTCACTACA	GTGATACAGA	TCACCTTTAT	CTTTCCCCCA	CACTCTATAC
1851	TCACCCTCCC	TACACTATAC	CATATTATTA	GITTCCGCCA	CAGICIAIAC
	TCAGGGTGCC	TAGAGTATAG	CATATIATIA	GGGTACTATT	ICITITECTA
1901	ICCIAGATAT	CCAACTAAGG	CTTCGGGACA	TGTTTTGAGC	GAAGATGGGT
1951	GTTTCTGCCC	GGATAGTATA	AATCGAGGAT	CCAGGTCTGG	GCAGATTCAA
200T	CCATGGGAGC	GAACACTTCA	AGAAAACCAC	CAGTGTTTGA	TGAAAATGAA
2051	GATGGTAAGA	AATATGGGAT	AGTGGCATAT	AAAAAATAGA	ATTTTGCAAA
2101	ATTCAAGTAT	<b>ATGCTTCTAG</b>	TTTCATAAGT	TAAGCATAAG	CATGGTCTGT
2151	AGGGCCTTGA	AGGAAAAAGG	CAAAGCTGCA	TGAGTGAGTC	TGAGGACTTT
2201	GTAGGCTCAT	AGCTAGGTTT	TACCTTCCAC	TTTCCATGGG	ACCTTTGGCA
2251	GCTTTCCTAA	<b>TCTCCACTAT</b>	ACCAATGTCC	TTTGTCCAAA	GGGAGCTGCA
2301		TGGTGGATAG			
2351	CCTTGGCAGT	TGAAGTTACC	CCCATTGCTC	ATTGTTACAG	ΔΔΔΔΤΔΓΔΤΤ
2401	ATCAACATGT	ACATGAATGA	TAACCAGTGC	TCATAATATT	ATAGAATGAA
2451	GCTGTGCCTT	CTGAATTTCC	AACTGCCAAG	CTTTTCTCTA	CTACACAAAT
2501	CCCATAATGC	TACGTCATAG	AAAAAAAAA	CACTTCTATT	CCACAAAACC
2551	CAAACTTTCC	ACCCCACACT	CACCAACACA	ACAATAAACC	GGAGAAAAGG
2221	CCTCATTCTC	AGGCCAGACT	CAGCAAGACA	AGAATAAAGG	CATGAGICCI
700T	TOTOGOTOT	CCATCAGTGA	GGCATGCTGG	AACTGGGCAA	TGCCTCCTCA
702T	IGICCCICIT	CCTTCCTATA	IGITAAGTCT	GAACAGCATT	GGCGTATGCA
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2751	AGGTAGTAAG	TTGTCCAGAC	CTCTGAGAGG	GAGCTCTTCC	GAGTAATTCC
2801	CAGAGAGCTC	TGCTAATTGG	AACAGGGAGG	AAAAGAATGG	ACTGAAATTC
2851	AGGAAATCTG	ACACCAGTCC	TACTACCAGT	TACTTGCTAG	GCCCAAGCAG
2901	CTTATTTACT	GACTCTATCT	TCAATTTTGT	TATCAATAAA	GTGAGGAGAT
2951	AGGTTCCTTC	CCACTCAAGA	AGTTTATCAT	TTTGAGATCC	TAAAGCAACT
3001	TTGTGAATTC	TGAAGAAGCT	TCTAAATCAT	CAAGGAAAGT	TTATTECETT
3051	AGAATGCAAG	TTTGATTGCT	GAAATGAAAA	CTACAAATAA	CAGTGGCTTA
		37,1301		CIACAMAIAA	CAGIGGETTA

TO THE STATE OF TH
3101 AGCCAAATGG AAATGTTTAT CTTTCTCATG TGACAATCTA GGCATAAGTA
2151 ATCCACCTCA TCTCTCCTTC CAGCAGCTTA GGGACICIGA CGCCAACIAC
2201 TTCCCTTTTT CCCTCTCTTC CCATTTCTAG AGIGGIACCC ICAGAGIGGC
2251 TAACCAACAC AACAATTCC AGCCAGTGAG AAAGGIGGAA AGIAGGAGAG
2201 CTTATCCCCA CTTATTTATA GGATTTGCTC IGGCIIGICA CIIICGIICA
2251 CTTCCACTTA CCTAGATACA AGAAAGACIG GGAAAIICAG IIIGIIAICI
2401 TOCCTOCCO TOACCTTCT AAAAATAAGG AGIICIGIII IAIIACAAAA
24E1 CAAAACAACA ATTAGGAGTT TGTCATGATT GGGGACAACT ACGICIGCIG
2501 TACTTCCCCC AAACAATCTT AGTTTTGAAT CIIGGGAIGG AAAIACIIII
2551 AAAAACAAA TATGGGCCAG GCGCGGTGGC TCACGCCTGT AATCCCAGCA
2601 CTTTGGGAGG CGAGGGGGG CGGATCACGA GGICAGAGA ICGAGACCAI
2651 CCTCCCTAAC ACGGTGAAAC CCCGTCTCTA CIAAAAAAIA CAAAAAAIA
2701 CCCCCCCTC CTCCTCCACG CCTGTAGTCC CAGCIACICG GGAGGCIGAG
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4051 CTTATCAAAT AGTAAAAGCA AAGATCTAGA GACTAGTGAT ATTACTTAAT
4101 TTTTCTGTCT CTAAAATGGA AAGACAAATA GGCTTGCTTT TCATTTAGTT
4151 GGTTTCCTCT GCTTCCTCTG GACTCAGAGC TAATGTTGTA CATGAGGCTG
4201 GTCGTCAGAG AATAGGGTGG AAAAGAGAGG CCAGCTGCAT ACTTTTAACT
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4251 TGCTGGGCTA CATTTGAAGG TAGTAGAATA GCATTATGAT GAGAAAACAC
4301 AGAAATGCAT AACTCTTCCT TGATTCAGCC AGGCTTTGTT CTTGCGGGAT
4351 GCCCAAGAAA GCTACATAAC CAAAGAATTG TGACAATTGG GAAATAAGAT
4401 ACCCTTTTT AGTTACTTTA AAGGACTCTA GAAAAACTAG GTTGAAGGAG
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4601 GGTGCTAGGC TCTCTGTCTG TTTATGCAGA CAGTTGCAAG GCAAAGGAAG
4651 TAGGAGGCA AGTCCACCTA CTATAAACCT GTCACTCTCT AGACATGAAG
4701 AATAGAGGAG GAAACAAGTT GGTCCTTGCT CTGTCATTGT GAACCCCATG
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ETEL TEATETTERA CACATAATTT TALLAGILAG LIAIGILGAL CILIAITEM
EOD1 CAAAACAAA GTAGGAGATT TTCAGGCTAG GCAIGGIIGC IIACGCCIGI
FOET AATOCOACOA CTTCAGGAGG CCGAGGGGGG CAGATCACGA GGTCAAGAGA
FOOT TOOMACONT COTEGOODAY ATGGTGAAAC CCCAICIUA CIAAAAAAA
FOR 1 CAAAAAAA T TAGCTGGGCA TGCCAGTGTG CGCCIGIAGI CCCAGCIAII
COOL CACCACCCTC ACCCACGAGA ATCTCTTGAA CCIGGGAGGI GAAGIIIGCA
COLL CTCACCTCAC ATTCCTCCAC TCCACTCCAG CCTGGCAACA GAGCAAGACI
C101 CTCTCCAAAA AAAACCCCCT TCCTTATTTC ATTATATAGAG ATATCTTCA
6101 CTGTCCAAAA AAAAACGGCT TGCTTATTTG ATTATAAAG ATATCTTTCA 6151 TAAATTAGAT CTCAAATTAT ACTATTGTTT TGCAGTTTTA GCTTTTATGT

6201	TTTAGGGCAA	ATCTTAAGTC	CTAATTACTT	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	ATTGTGGTAA
6251	AATGTATATA	ACAAAATGTA	CCATTTAATC	ATTTTAGAAT	ATACGGTTTA
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				TTCATTTAGC	
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6701	TATAAACATT	CCTCTCCAAA	TATCTCTTCA	AGTCCCTGTT	TTCAATTCTT
				GATCATATAA	
				TACCTAATTA GGCTAGAGTA	
0001	ITTAGTAATG	GGACACAGCC	CCTCTCCCAC	CTCCCACTAA	TCTACATCTT
				GTGCCAGTAA	
				TGGTCAACCA	
				TCTAAGGAAA	
				ACTAATGAAT	
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7151	AGGTAATAAT	TGGGCATACT	TCATTAGGTC	TTTGTGAGGA	TTGAATAAAT
7201	AATGCAAGTA	AAACACTTAG	CAAAGTATTT	CCCATAAAGT	AACCACTCAA
7251	TTAATGCTAA	TTAAGTGTTA	TTTACTAACA	TCAGAGTTTC	CTAGTGTGAA
7301	CTCTTTGAAG	<b>TACTTTAAGT</b>	<b>TCTGAGAAAA</b>	ACAAAATTAA	TTAAATGCAA
7351	CTCTGTCGAT	<b>TCCACAGTTA</b>	<b>ATTAGACCTA</b>	TTCATGTTTC	TATTGACTGG
7401	ATTAACAGAA	CGGCAGATTT	<b>TATGGATTCT</b>	GTTAAAACCT	ATATAAAAAC
7451	ACTITAAAAG	AAGCCAAGTT	<b>ATTGACTGCA</b>	CAAAAACATA	ATCTCATCTG
				GTTTTGTTT	
				GTTTACTTTG	
				TGATCAACAG	
				ATATTCTGAG	
				AATAAAAGAA	
				TTTTTAAAA	
				TIGTITGTT	
				GGCTGATTTA	
7901	ATTITIACAG	GAGAGAGIGG	ACTIGITIAC	AATTCAGAGT	AACTTTATAC
				ATGTGTATCC	
				GTTAAATCAA	
8021	TCTTCTAGAA	TATTATAGCT	AAGAAAAIII	GGACTTAAGT	TIAAAAAGCI
8101	GCTCTAAAGA	GTTCATCAAT	GCCCTGAGTT	TGCAGAGAGT	TCAATTATTG
				TGTTCTACTT	
				CAGTTTTCCA	
				TGGGCCAAGA	
8301	CAGATTTGCA	ATCCAAAAGA	AATAGGAGGT	TGCTAAATTG	ATTCCAGCTA
				TGACTGTCTA	
				TCCGACTTTC	
8451	CTTGAGTAAT	GCTGTCTCGT	ATTTATTATT	TTGCATTAGA	ATGGTTGGAA
				TGGCTTCTTA	
8551	TCATCTTGGA	CAACCTAACA	TTTAGTAAAG	GCATTTGTCA	TAAATAACCT
8601	CAAGTCCAAT	TTATGGCAAG	GGTTTTAATT	TGTAAGGGCT	TTATTTCTCC
8651	ATACAAAGGG	ATTGGAGAAA	CAAACTAGAA	AGCCAGAAAA	CAGACCACAA
				TCCCTGAGCA	
				AATTTAGGAA	
8801	TGCCTTTAGA	GCTTCCAGTG	TTTGTTAGCA	TATTAAAGTC	TCTGAAATGA
8851	CCTACAATAT	TGAAATCTCA	GTCTTCTGCT	ΑΤΤΙΤΙΑΑΤΔ	TTTATTTCAA
8901	ΔΔΤΩΔΔΑΤΛΛ	TTTTTGTGAA	ΔΔΔCΔΤΤΤΤΔ	ATGTCTGTGG	CTCATAATAT
					ATCTACTCTT
9001	TATCTCTTCC	AAACATCTTT		. דדררדהרדהה דדררדהרדהר	TTTAATGGCA
					TGAAAAAATG
0101	. ACAMAIIIII Taattiiii	AAADIDIAAA TATACACCAT	CAAAACTCCT	TATECTCCTC	TGTAAGTTTT
2101	TCCTTACAAC	ATTACACGAT	CCATAATTA	TATOCICCIC	GTTTAATGAG
0201 2T2T	TACAACACA	CATACCTCAC	TTTAATTCTC	CONTESTOR	TGTTTCTAGT
9201	TALAACACAA	CTTCCATTTC	ATCAAAATT	ATTCCTTCTT	TATGATTTT
2727	. TAAAGTACAA	GIIGGAIIIG	AIGAAAAIIC	. ATTOCTICIT	IAIGAIIIII

9301 TAAAACTCAA GAACATGTTA GTTAAAGAGT GTCTTCTGAA CAAATTCTTG
0251 TCAACTACTT CCTGATTATT AAGTAACACT CATGCIACCG IAACIIIIA
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OAEL CTTCAAAAT TAAATCTGCA AGCCAGTTTC ATTAITCAGA CAATTIGGT
OSOL ATCACTTCAA GCCTACTATC TTCAAAGAAA ATGGGAGIGC AGGCCIICAI
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INCOL XXXXXXXXX CTCTXXXXXC (ALICITAGI ICALGAGCIA IACAAAAA
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12401	ΤζΔΑΤΑΤΑΑΑ	ATAATTAGGT	GTTACTGATG	GCTTGAATGT	GGGGTAAGAT
12/51	GGAAAGAACA	ΔΔΔΤCΔΔGGA	TAAATCCTAG	GTTTTTGCTT	GAGTAGTTAT
12501	CTCCATCACT	CTCACATTTT	ACTAAGATGG	AGATGCGTGG	GAACGGAGGG
T720T	GIGGAIGACI	CTCCTCACAT	ACACTCTACA	GTTCACTTTT	GGAGGCATAC
T522T	GTTTGGGACC	CIGCICACAI	ACAGICIAGA	CAACTACCAC	CTCCACTACA
12601	AGTGATTATG	GGACAGCTAA	ATGATGGTGC	CAAGTAGGAG	CIGGAGIAGA
12651	<b>GTATCCAGCA</b>	ATGAGTGGAA	ACATCTGGGA	TGGAGACAGA	AAGACACGGG
12701	TATTAATTCT	ACGGGGATGG	CTAAGTCTGC	TCTGAGAGAC	AGTGTGGAGA
12751	CCAACGAGAA	CACCAATCCT	ΔΔΤΔΤΤΤΔGΔ	AACAAGGCAG	TGGATAGCAA
12/01	CCAAGGAGAA	CAAACTCCAA	CCAAACACAT	AGTTGATCAT	CCAGTTCAAC
T580T	ICIAGCIAIG	GAAAGTGGAA	GGAAAGAGAT	ATCCTTCTCT	CTCACTAACT
12851	ACTACTCTTG	TTGTAGTTCA	CHAIGHIGA	ATGCTTCTGT	TTCCTATTCA
12901	CGGTGAGAAA	AATCTATGGG	AGTAGGCAAC	ATGGAGGATG	TIGGIATICA
12951	CAAAAGCAGT	TTAGTGGAGT	GTGGAGGCCT	GAGCCAGACT	AGAATGAGTT
13001	ACCACTACAT	GGAAGATAAG	AATGCAGATA	TGGGCCCAGC	GCGGTGGCTC
13001	ACCCCTCTAA	TCCCACCACT	TTGGGAGGCC	AAGGTGAGCA	GATCACAAGG
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13151	AAAAATACAA	AAAATTAGCC	GGGCCTGGTG	GCGGGTGCCT	GIAGICCCAG
13201	CTACTCGGGA	GGCTGAGGCA	GGAGAATGGC	GTGAACCCGG	GAGGTGGAGC
13251	TGGCAGTGAG	CCGAGATGGT	GCCACTGCAC	TCCAGCCTGG	GCAACAGAGC
12201	AACACTCCAT	CTCAAAAAA	ΔΔΔΔΔΔΔΔΔ	AAGAATGCAG	ATATGGCAAG
12201	TATACACAAC	CTTCAACAAC	TTTCCTCTAA	AAGGAAGCGG	ΔGΔΔΔΤΔΑΑС
T332T	TATAGACAAG	CTTCAAGAAG	AATTCACCTA	AATCTAATAT	AATGGATTIT
13401	AAAGAGATGA	IGCCIAAIAI	AATTCAGCTA	AATGTAATAT	AATTCCCTCC
13451	TTTAAGATGA	GGTACTAGAG	CATGTAATAT	AAATCTATTA	AATTGGGTGG
13501	CCAGGAACCA	GGACTGGCTC	ATCAGCATGG	ACCAGGCTAG	ACGCACAGGG
13551	CCTTATATCC	AGAAGGACAT	CACCTTTGGG	TTTTAATGCT	CTGCACTIGC
13601	TGTCTCCAAA	TTCTAACTGT	CTCTTAGGCT	CTCATCAACA	CCCACCTCCA
13651	TATCCACATA	TTCACTACCT	CAGGGAGTTC	AATTTGGAAG	CAAATGATGT
T202T	TATCCAGATA	TTTACTATCC	ACTAACATTC	TTGTTAGGGA	CTCTTCCCAG
T3\0T	GAAAAIGIAC	HITACIATCO	AGTAACATTC	CATTOCATCA	CTCTACAATT
13751	AGATTGTCGA	ACAACCATAA	TGCATITIAT	CATTCGATCA	GICTACAATT
13801	TAAACATAGO	AGGACTGGAC	AGAGGCACAG	GAAGATTAAG	CCACTGACCT
13851	TAAGTCAGAC	AGTCACATGG	GTAGATCCGG	AATCTTGATC	TAAAATGAAT
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13931	CATCAACAC		CCTAACTCTA	AATCTTACTT	TCAGAGAGCT
14001	CATCAAACAC	TCATTAIGIG	CTCACATTCA	TCTTCCCTTC	TECCETAACT
14051	. AAAAACAATI	TCATTTCACA	GIGACATICA	TCTTCGCTTC	CCCCCCTTCC
14101	. CACATGCATA	TGCCTTAGAC	CACATTATTA	ATGAAGTATT	TCA CCA CCA C
14151	. ATCTAGAGCA	CCTTTTCTTC	CCTGGAGTTA	ATCATCCAGT	TCAGCACCAC
14201	TCTTGAGCTT	TGCTTAGCTT	CTTCTACCCA	\ TTTGGATTTT	AAGGACAACA
14251	ΑΤΤΟΟΔΑΤΘΟ	CCTTTATCCA	TGTATTTAAC	: AATTCATTAT	GAGCCAGGIG
1/2/1	AAGTGGATCA	CACCTCTAAT	CCCAACACTT	TGGGAGGCTG	AGGCAGGTGG
14361	ATCCCTCCAC	CCCAGGAGTT	CACAACCAGO	CTGGGCAACA	TGGTGAGACT
14331	. ATCGCTGGAG	CCCAGGAGII		GGGTATGGTG	GCAGGAGATC
14401	CCATCICIAC	. CAIIIIIII	TTOCACCACT	CCACACTACC	CTCCCCAACA
14451	L AAGGCTACGC	TGAGCIGIAA	LIGCACCAC	GCACACTAGC	TCATCATCAT
14501	L GAGCAAGAC(	CTGTCTCACC	; aaaaacaaa <i>a</i>	ACAATTTATT	ICAICAICAI
14551	TGTCATCAT	ATTGTCACTO	CTCACTCTT	AACATITIII	AGGICAACII
14601	Ι ΔΔΤΤΔΔΤΔΤ(	ATACCTTGTG	GGATAATTT	TATTTATTTT	TATAAAATAT
1/651	TGAAGTTTT	GCCACTTTGA	TAACTTCTT	ATTITCTGTC	CAGAGTATAA
14701	CATACCACC	- AAAAGGCTCT	ΔΔΔΔΤΔΔGG	TTGAGGTATT	AAAAAGATCT
1470	L CATACCAGG	- TCTTATCTT	CTAATCAAT	ACTAGAATTG	GCCTGATTGC
14/5.	LICIGITIAA	CONTRACTO	CTACTCCTC	A TATCATATCO	ACCUTATION
1480	L TTTCCTCAG	r GGGTTTTCTC	GIAGICCIG/	TATGATATCG	TOTOATATAA
1485	L ATAGTCCTG/	A AATATCCTAT	CATTAACAT	T TGTGGTGGTA	ICIGATATAA
14901	1 AGGTAGATG	A ACTTCATTGO	AGCTATTCT	T AGGAAATGCG	TATTIAAATG
1495	1 CATAGTTAA	A AGCAAGATT	r acaattata	G AAGGAATGCA	AATGAGTIGI
1500	1 AGAAAGCTC	Α ΤΔΔΔΔΤΔΔΔ	ATCAAGAAG	A AAGAATTACC	CATCATGCCT
1500.	1 CACCCCACT	~ 17070717070	CTAATATTT	T TGGCTGTTTT	CATTTGCAAC
1202	L CAGCCCAGI	A TTOTACCACT	CIAMIMIII	T CCTACCCACT	ATGTTTTTCA
T210	CCCATCICC	A TICTAGCAGG	TACTTACE	1 CCIACCCACI	ATGTTTTCA
1515	L CTATATTTC	T TGTTTAAAT	I IACITAATT	A TITGTTAATT	AIGITITICE
1520	1 TCTCACTAG	A AAGTGAACT	C CATGAGGGC	C AGGGAIIIII	GCTATTTTGT
1525	1 TCACTTTTG	T ATCCTTAGC	A CCTACTTTG	T TGATTAAGTO	AATGCATTAA
1530	1 TGATCTATT	T TTAATCTGT	G TATGTGTAT	A AAAGACACTI	GATAIAICIG
1525	1 GGATGATAT	Τ ΓΔΔΤΔΤΔΓΤ	T TTGTATCCT	C ATTTTCACCA	A TAGGTAGIII
1510	1 ATCTCAATT	CTTGAAATT	T GTTGATTTT	C TTGAATAATT	TAGCAGTTGT
T240	1 ACAATTCT	A AACATAAAT	, GIIGAIIII A TAATTTCCT	T AAATATACAT	ACCATTTAA
1545	T ACAATICIA	A AACATAAAT	A TAATTIGET	. ~~	ACCALLIAN

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15601 ACACATGAAT ATTTCTTTTG GAGTATTTAA ATCAICICIG CAAIAAICCI
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19401 GAAAAGGGGA AGAAATTGA GAGTTGAGC AGCTGGGGGG AGGGCTGTCT 19451 TAGATAATAA CCTGTATAGG TTTAGCTGAC AGCTGGGGGG AGGGCTGTCT
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AACCA AAA—TCCCCCT CTTTATTCAA ALIILILIIII ALIAAAIUUI CCCCCCI CTTTATTCAA AIIILILIIII ALIAAAIUUI CCCCCCI
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24704					
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21751	GGTTACTGGG	TTAAGGATTT	TTGATAGGAA	GGCTACTGGT	TGTCAGTGGC
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21951	GGTACATGTG	CACAACGTGC	<b>AGGTTTGTTA</b>	CATATTTATA	CATGTGCCAC
	GTTGGTGTGC				
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	TCTGACTCCC				TCTGCCTCTC
	TCCTCTCTGT			TCCTGTTTCT	
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22251	CTCCTGTCTC	TCTCTTTCTC	TCTCCTCTCT	CTCTCTCCCC	
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	TGTGTCTCTT				TCTTTGTCCT
22331	CTCTCTTTCT	CTCTCCTCTC	TCTCCTCTCT	CTCTCTCCCC	
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23251 23301 23351 23401	NNNNNNNNN NNNNNNNNN AAAGGTTGCT GAACATACTG	NNNNNNNNN NNNNNNNNN TTACGAGGAA ACATATTAAT	NNNNNNNNN NNNNNNNNN GTTAAATTTA TCTTTGAAAA	NNNNNNNNN NNNNNNNNN AAAGTAGAAG GAAATTTATA	NNNNNNNN NNNNNNAAA GCAAAGAATT ACTGATATCT
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23251 23301 23351 23401 23451 23501 23551 23601 23701 23751 23751 23801	NNNNNNNN NNNNNNNNN AAAGGTTGCT GAACATACTG AACACTGAAG GAGCATAGCA ACAAGTAGGA TGTATTTGAA AGTCCATGCT ATTCATAGTT CTTAGCACTG GAGAGTGACC	NNNNNNNN NNNNNNNNN TTACGAGGAA ACATATTAAT GAGGCTTATG TCTTTTATTT TTATGAGGAA TTATTTTTTC ATCCCCCCA GCCTTAGGAT AATCAGAGAG GATGCTGTAC	NNNNNNNN NNNNNNNNN GTTAAATTTA TCTTTGAAAA CTTAGGGTTT AGAAGAAAT CCCTGAAAAT TCTTTGGAAA AGCTAAGACT ACATTTATAG AAAACTTGAG AAGAGTAGGT	NNNNNNNN NNNNNNNNN AAAGTAGAAG GAAATTTATA TATGTTAGGA TAATTCTTAA TATATACAAA AGGCATGTTAT GCTTCTGCTC GGGACCCTCA AGGCATTTGC CTCGAAATGT	NNNNNNNN NNNNNNAAA GCAAAGAATT ACTGATATCT GTTTGGTTTA TATGGAATTC GTTTATTTTG TCACCAAAGG ATCCTCAGCG ATCCTCAGCG ATTTTAAAAA GAGGTTAAAT GGTACTTTTC
23251 23301 23351 23401 23451 23501 23551 23601 23751 23751 23751 23801 23851	NNNNNNNN NNNNNNNNN AAAGGTTGCT GAACATACTG AACACTGAAG GAGCATAGCA ACAAGTAGGA TGTATTTGAA AGTCCATGCT ATTCATAGTT CTTAGCACTG GAGAGTGACC TTGGGTTATC	NNNNNNNN NNNNNNNNN TTACGAGGAA ACATATTAAT GAGGCTTATG TCTTTTATTT TTATGAGGAA TTATTTTTC ATCCCCCCA GCCTTAGGAT AATCAGAGAG GATGCTGTAC TCGTCTTATT	NNNNNNNN NNNNNNNNN GTTAAATTTA TCTTTGAAAA CTTAGGGTTT AGAAGAAAT CCCTGAAAAT TCTTTGGAAA AGCTAAGAT ACATTTATAG AAAACTTGAG AAGAGTAGGT CTCATCACAA	NNNNNNNN NNNNNNNNN AAAGTAGAAG GAAATTTATA TATGTTAGAA TAATTCTTAA TATATACAAA AGGCATGTAT GCTTCTCTC GGGACCCTCA AGGCATTTGC CTCGAAATGT ATGGTGAAGA	NNNNNNNNN NNNNNNAAA GCAAAGAATT ACTGATATCT GTTTGGTTTA TATGGAATTC GTTTATTTTG TCACCAAAGG ATCCTCAGCG ATTTTAAAAA GAGGTTAAAT GGTACTTTTC AATGGTCAGC
23251 23301 23351 23401 23451 23501 23551 23601 23751 23751 23801 23851 23801	NNNNNNNN NNNNNNNNN AAAGGTTGCT GAACATACTG AACACTGAAG GAGCATAGCA ACAAGTAGGA TGTATTTGAA AGTCCATGCT ATTCATAGTT CTTAGCACTG GAGAGTGACC TTGGGTTATC CACATTAAAG	NNNNNNNN NNNNNNNNN TTACGAGGAA ACATATTAAT GAGGCTTATG TCTTTTATT TTATGAGGAA TTATTTTTC ATCCCCCCA GCCTTAGGAT AATCAGAGAG GATGCTGTAC TCGTCTTATT AGCAGATACT	NNNNNNNN NNNNNNNNN GTTAAATTTA TCTTTGAAAA CTTAGGGTTT AGAAGAAAT CCCTGAAAAT TCTTTGGAAA AGCTAAGACT ACATTTAG AAAACTTGAG AAAACTTGAG AAGAGTAGGT CTCATCACAA GAGATTCAGC	NNNNNNNN NNNNNNNNN AAAGTAGAAG GAAATTTATA TATGTTAGGA TAATTCTTAA TATATACAAA AGGCATGTAT GCTTCTCCTC GGGACCCTCA AGGCATTTGC CTCGAAATGT ATGGTGAAGA AAGTGAGAAA	NNNNNNNNN NNNNNNAAA GCAAAGAATT ACTGATATCT GTTTGGTTTA TATGGAATTC GTTTATTTTG TCACCAAAGG ATCCTCAGCG ATTTTAAAAA GAGGTTAAAT GGTACTTTTC AATGGTCAGC ACCTGTCCTG
23251 23301 23351 23401 23451 23501 23651 23651 23751 23801 23851 23901 23951	NNNNNNNN NNNNNNNNN AAAGGTTGCT GAACATACTG AACACTGAAG GAGCATAGCA ACAAGTAGGA TGTATTTGAA AGTCCATGCT ATTCATAGTT CTTAGCACTG GAGAGTGACC TTGGGTTATC CACATTAAAG GTTCACACAG	NNNNNNNN NNNNNNNNN TTACGAGGAA ACATATTAAT GAGGCTTATG TCTTTTATTT TTATGAGGAA TTATTTTTC ATCCCCCCA GCCTTAGGAT AATCAGAGAG GATGCTGTAC TCGTCTTATT AGCAGATACT CCAGGAAGAG	NNNNNNNN NNNNNNNNN GTTAAATTTA TCTTTGAAAA CTTAGGGTTT AGAAGAAAT CCCTGAAAAT TCTTTGGAAA AGCTAAGACT ACATTTATAG AAAACTTAGA AAAACTTAGA AAGAGTAGGT CTCATCACAA GAGATTCAGC GCAGAGGCAG	NNNNNNNN NNNNNNNNN AAAGTAGAAG GAAATTTATA TATGTTAGGA TAATTCTTAA TATATACAAA AGGCATGTAT GCTTCTGCTC GGGACCCTCA AGGCATTTGC CTCGAAATGT ATGGTGAAGA AAGTGAGAAA AATCCTCACC	NNNNNNNNN NNNNNNAAA GCAAAGAATT ACTGATATCT GTTTGGTTTA TATGGAATTC GTTTATTTTG TCACCAAAGG ATCCTCAGCG ATTTTAAAA GAGGTTAAAT GGTACTTTTC AATGGTCAGC ACCTGTCCTG CCACTTCTGT
23251 23301 23351 23401 23451 23501 23551 23601 23701 23751 23851 23801 23951 23951 24001	NNNNNNNN NNNNNNNNN AAAGGTTGCT GAACATACTG AACACTGAAG GAGCATAGCA ACAAGTAGGA TGTATTTGAA AGTCCATGCT ATTCATAGTT CTTAGCACTG GAGAGTGACC TTGGGTTATC CACATTAAAG GTTCACACAG TTGCCTCCAA	NNNNNNNN NNNNNNNNN TTACGAGGAA ACATATTAAT GAGGCTTATG TCTTTTATTT TTATGAGGAA TTATTTTTC ATCCCCCCA GCCTTAGGAT AATCAGAGAG GATGCTGTAC TCGTCTTATT AGCAGATACT CCAGGAAGAG AGCTCAAGGA	NNNNNNNN NNNNNNNNN GTTAAATTTA TCTTTGAAAA CTTAGGGTTT AGAAGAAAT CCCTGAAAAT TCTTTGGAAA AGCTAAGACT ACATTTATAG AAAACTTGAG AAAACTTGAG AAGAGTAGGT CTCATCACAA GAGATTCAGC GCAGAGGCAG GAGTGAGCTT	NNNNNNNN NNNNNNNNN AAAGTAGAAG GAAATTTATA TATGTTAGGA TAATTCTTAA TATATACAAA AGGCATGTAT GCTTCTGCTC GGGACCCTCA AGGCATTTGC CTCGAAATGT ATGGTGAAGA AAGTGAGAAA AAGTGAGAAA AATCCTCACC TACCCTTCAT	NNNNNNNNN NNNNNNAAA GCAAAGAATT ACTGATATCT GTTTGGTTTA TATGGAATTC GTTTATTTTG TCACCAAAGG ATCCTCAGCG ATTTTAAAAA GAGGTTAAAT GGTACTTTTC AATGGTCAGC ACCTGTCCTG CCACTTCTGT ATTTACTCAT
23251 23301 23351 23401 23451 23501 23651 23651 23701 23751 23751 23851 23901 23951 24001 24051	NNNNNNNNN NNNNNNNNN AAAGGTTGCT GAACATACTG AACACTGAAG GAGCATAGCA ACAAGTAGGA TGTATTTGAA AGTCCATGCT ATTCATAGTT CTTAGCACTG GAGAGTGACC TTGGGTTATC CACATTAAAG GTTCACACAG TTGCCTCCAA CCTCTTACTA	NNNNNNNN NNNNNNNNN TTACGAGGAA ACATATTAAT GAGGCTTATG TCTTTTATTT TTATGAGGAA TTATTTTTC ATCCCCCCA GCCTTAGGAT AATCAGAGAG GATGCTGTACT TCGTCTTATT AGCAGATACT CCAGGAAGAG AGCTCAAGGA ATTTGACTCT	NNNNNNNN NNNNNNNNN GTTAAATTTA TCTTTGAAAA CTTAGGGTTT AGAAGAAAT CCCTGAAAAT TCTTTGGAAA AGCTAAGACT ACATTTATAG AAAACTTGAG AAGAGTAGGT CTCATCACAA GAGATTCACA GCAGAGGCAG GAGTGAGCTT TAAGATAATC	NNNNNNNN NNNNNNNNN AAAGTAGAAG GAAATTTATA TATGTTAGGA TAATTCTTAA TATATACAAA AGGCATGTAT GCTTCTGCTC GGGACCCTCA AGGCATTTGC CTCGAAATGT ATGGTGAAGA AAGTGAGAAA AAGTCCTCAC TACCCTTCAT CTGAGATTTA	NNNNNNNNN NNNNNNAAA GCAAAGAATT ACTGATATCT GTTTGGTTTA TATGGAATTC GTTTATTTTG TCACCAAAGG ATCCTCAGCG ATTTTAAAAA GAGGTTAAAT GGTACTTTTC AATGGTCAGC ACCTGTCCTG CCACTTCTGT ATTTACTCAT AACCAGAAAA
23251 23301 23351 23401 23451 23501 23651 23651 23701 23751 23851 23901 23951 24001 24051 24101	NNNNNNNN NNNNNNNNN AAAGGTTGCT GAACATACTG AACACTGAAG GAGCATAGCA ACAAGTAGGA TGTATTTGAA AGTCCATGCT ATTCATAGTT CTTAGCACTG GAGAGTGACC TTGGGTTATC CACATTAAAG GTTCACACAG TTGCCTCCAA CCTCTTACTA CTATTATGAT	NNNNNNNN NNNNNNNNN TTACGAGGAA ACATATTAAT GAGGCTTATG TCTTTTATTT TTATGAGGAA TTATTTTTC ATCCCCCCA GCCTTAGGAT AATCAGAGAG GATCCTTATT AGCAGATACT CCAGGAAGAG AGCTCAAGGA ATTTGACTCT CCCCTTATTT	NNNNNNNN NNNNNNNNN GTTAAATTTA TCTTTGAAAA CTTAGGGTTT AGAAGAAAT CCCTGAAAAT TCTTTGGAAA AGCTAAGACT ACATTTATAG AAAACTTGAG AAGAGTAGGT CTCATCACAA GAGATTCAGC GCAGAGGCAG GAGTGAGCTT TAAGATAATC GAATGAGAAT	NNNNNNNN NNNNNNNN AAAGTAGAAG GAAATTTATA TATGTTAGGA TAATTCTTAA TATATACAAA AGGCATGTAT GCTTCTGCTC GGGACCCTCA AGGCATTTGC CTCGAAATGT ATGGTGAAGA AAGTGAGAAA AATCCTCAAC TACCCTTCAT CTGAGATTTA ATATGTCTAA	NNNNNNNNN NNNNNNAAA GCAAAGAATT ACTGATATCT GTTTGGTTTA TATGGAATTC GTTTATTTTG TCACCAAAGG ATCCTCAGCG ATTTTAAAAA GAGGTTAAAT GGTACTTTTC AATGGTCAGC ACCTGTCCTG CCACTTCTGT ATTTACTCAT AACCAGAAAA AAATGATTT
23251 23301 23351 23401 23451 23501 23551 23601 23751 23751 23851 23901 23951 24001 24051 24151	NNNNNNNN NNNNNNNNN AAAGGTTGCT GAACATACTG AACACTGAAG GAGCATAGCA ACAAGTAGGA TGTATTTGAA AGTCCATGCT ATTCATAGTT CTTAGCACTG GAGAGTGACC TTGGGTTATC CACATTAAAG TTGCCTCCAA CCTCTTACTA CTATTATGAT TAAAAACACT	NNNNNNNN NNNNNNNNN TTACGAGGAA ACATATTAAT GAGGCTTATG TCTTTTATTT TTATGAGGAA TTATTTTTC ATCCCCCCA GCCTTAGGAT AATCAGAGAG GATGCTGTAC TCGTCTTATT AGCAGATACT CCAGGAAGAG AGCTCAAGGA ATTTGACTCT CCCCTTATTT ATTAAAGGTC	NNNNNNNN NNNNNNNNN GTTAAATTTA TCTTTGAAAA CTTAGGGTTT AGAAGAAAT CCCTGAAAAT TCTTTGGAAA AGCTAAGACT ACATTTATAG AAAACTTGAG AAGAGTAGGT CTCATCACAA GAGATTCAGC GCAGAGGCAG GAGTGAGCTT TAAGATAATC GAATGAGAAT ACAAAGCCAG	NNNNNNNN NNNNNNNNN AAAGTAGAAG GAAATTTATA TATGTTAGGA TAATTCTTAA TATATACAAA AGGCATGTAT GCTTCTGCTC GGGACCCTCA AGGCATTTGC CTCGAAATGT ATGGTGAAGA AAGTGAGAAA AATCCTCACC TACCCTTCAT CTGAGATTTA ATATGTCTAA TGAATGATAA	NNNNNNNNN NNNNNNAAA GCAAAGAATT ACTGATATCT GTTTGGTTTA TATGGAATTC GTTTATTTTG TCACCAAAGG ATCCTCAGCG ATTTTAAAAA GAGGTTAAAT GGTACTTTTC AATGGTCAGC ACCTGTCCTG CCACTTCTGT ATTTACTCAT AACCAGAAAA AAATGATTT AGGGATTGGT
23251 23301 23351 23401 23451 23501 23551 23601 23751 23751 23801 23951 23951 24001 24051 24151 24201	NNNNNNNN NNNNNNNNN AAAGGTTGCT GAACATACTG AACACTGAAG GAGCATAGCA ACAAGTAGGA TGTATTTGAA AGTCCATGCT ATTCATAGTT CTTAGCACTG GAGAGTGACC TTGGGTTATC CACATTAACAG GTTCACACAG GTTCACACAG CTCTCCAA CCTCTTACTA CTATTATGAT TAAAAACACT ACCTCTGGCT	NNNNNNNN NNNNNNNNN TTACGAGGAA ACATATTAAT GAGGCTTATG TCTTTTATTT TTATGAGGAA TTATTTTTC ATCCCCCCA GCCTTAGGAT AATCAGAGAG GATGCTGTAC TCGTCTTATT AGCAGATACT CCAGGAAGAG AGCTCAAGGA ATTTGACTCT CCCCTTATT ATTAAAGGTC CCTATATTA	NNNNNNNN NNNNNNNNN GTTAAATTTA TCTTTGAAAA CTTAGGGTTT AGAAGAAAT CCCTGAAAAT TCTTTGGAAA AGCTAAGACT ACATTTATAG AAAACTTGAG AAGAGTAGGT CTCATCACAA GAGATTCAGC GCAGAGGCAG GAGTGAGCTT TAAGATAATC GAATGAGAAT ACAAAGCCAG GTTCATCCTT	NNNNNNNN NNNNNNNNN AAAGTAGAAG GAAATTTATA TATGTTAGGA TAATTCTTAA TATATACAAA AGGCATGTAT GCTTCTGCTC GGGACCCTCA AGGCATTTGC CTCGAAATGT ATGGTGAAGA AAGTCGTCACC TACCCTTCAT CTGAGATTTA ATATGTCTAA TGAATGATAA CAAAGAACAA	NNNNNNNNN NNNNNNAAA GCAAAGAATT ACTGATATCT GTTTGGTTTA TATGGAATTC GTTTATTTTG TCACCAAAGG ATCCTCAGCG ATTTTAAAAA GAGGTTAAAT GGTACTTTTC AATGGTCAGC ACCTGTCCTG CCACTTCTGT ATTTACTCAT AACCAGAAAA AAATGATTTT AGGGATTGGT AAATAGCCCC
23251 23301 23351 23451 23451 23501 23551 23601 23751 23851 23901 23951 24901 24051 24151 24201 24251	NNNNNNNNN NNNNNNNNN AAAGGTTGCT GAACATACTG AACACTGAAG GAGCATAGCA ACAAGTAGGA TGTATTTGAA AGTCCATGCT ATTCATAGTT CTTAGCACTG GAGAGTGACC TTGGGTTATC CACATTAACAG GTTCACACAG TTGCCTCCAA CCTCTTACTA CTATTATGAT TAAAAACACT ACCTCTGGCT CATTTATTGA	NNNNNNNNN NNNNNNNNN TTACGAGGAA ACATATTAAT GAGGCTTATG TCTTTTATTT TTATGAGGAA TTATTTTTC ATCCCCCCA GCCTTAGGAT AATCAGAGAG GATGCTGTAC TCGTCTTATT AGCAGATACT CCAGGAAGAG AGCTCAAGGA ACTTGACTCT CCCCTTATT ATTAAAGGTC CCCTTATT ATTAAAGGTC CCTATAGTTA GTGCCTACTA	NNNNNNNN NNNNNNNNN GTTAAATTTA TCTTTGAAAA CTTAGGGTTT AGAAGAAAT CCCTGAAAAT TCTTTGGAAA AGCTAAGACT ACATTTATAG AAAACTTGAG AAGAGTAGGT CTCATCACAA GAGATTCAGC GCAGAGGCAG GAGTGAGCTT TAAGATAATC GAATGAGAAT ACAAAGCCAG GTTCATCCTT AACTCTAGAT	NNNNNNNN NNNNNNNN AAAGTAGAAG GAAATTTATA TATGTTAGGA TAATTCTTAA TATATACAAA AGGCATGTAT GCTTCTGCTC GGGACCCTCA AGGCATTTGC CTCGAAATGT ATGGTGAAGA AATCCTCACC TACCCTTCAT CTGAGATTTA ATATGTCTAA TGAATGATAA CAAAGAACAA ATGTTTTTAA	NNNNNNNNN NNNNNNAAA GCAAAGAATT ACTGATATCT GTTTGGTTTA TATGGAATTC GTTTATTTTG TCACCAAAGG ATCCTCAGCG ATTTTAAAAA GAGGTTAAAT GGTACTTTTC AATGGTCAGC ACCTGTCCTG CCACTTCTGT ATTTACTCAT AACCAGAAAA AAATGATTTT AGGGATTGGT AAATAGCCCC TATATGCTAT
23251 23301 23351 23451 23451 23501 23551 23601 23751 23851 23901 23901 24901 2401 24151 24201 24251 24301	NNNNNNNNN NNNNNNNNN AAAGGTTGCT GAACATACTG AACACTGAAG GAGCATAGCA ACAAGTAGGA TGTATTTGAA AGTCCATGCT ATTCATAGTT CTTAGCACTG GAGAGTGACC TTGGGTTATC CACATTAAAG GTTCACACAG TTGCCTCCAA CCTCTTACTA CTATTATGAT TAAAAACACT ACCTCTGGCT CATTTATTA CTATTTATTA	NNNNNNNNN NNNNNNNNN TTACGAGGAA ACATATTAAT GAGGCTTATG TCTTTTATTT TTATGAGGAA TTATTTTTC ATCCCCCCA GCCTTAGGAT AATCAGAGAG GATGCTGTAC TCGTCTTATT AGCAGATACT CCAGGAAGAG AGCTCAAGGA ATTTGACTCT ATTAAAGGTC CCCTTATTT ATTAAAGGTC CCTATATT ACTACACA ACCTACCACA	NNNNNNNN NNNNNNNNN GTTAAATTTA TCTTTGAAAA CTTAGGGTTT AGAAGAAAT CCCTGAAAAT TCTTTGGAAA AGCTAAGACT ACATTTATAG AAAACTTGAG AAGAGTAGGT CTCATCACAA GAGATTCAGC GCAGAGGCAG GAGTGAGCTT TAAGATAATC TAAATGAGAAT ACAAAGCCAG GTTCATCCTT AACTCTGAT TTCCTGTAAG	NNNNNNNNN NNNNNNNNN AAAGTAGAAG GAAATTTATA TATGTTAGGA TAATTCTTAA TATATACAAA AGGCATGTAT GCTTCTGCTC GGGACCCTCA AGGCATTTGC CTCGAAATGT ATGGTGAAGA AATCCTCACC TACCCTTCAT CTGAGATTTA ATATGTCTAA TGAATGATAA CAAAGAACAA ATGTTTTTAA GTAGGTATCA	NNNNNNNNN NNNNNNAAA GCAAAGAATT ACTGATATCT GTTTGGTTTA TATGGAATTC GTTTATTTTG TCACCAAAGG ATCCTCAGCG ATTTTAAAAA GAGGTTAAAT GGTACTTTTC AATGGTCAGC ACCTGTCCTG CCACTTCTGT ATTTACTCAT AACCAGAAAA AAATGATTTT AGGGATTGGT AAATAGCCCC TATATGCTAT TTCATTATAC
23251 23351 23451 23451 23551 23551 23601 23751 23751 23751 23751 23851 24051 24051 24151 24251 24251 24251 24351	NNNNNNNN NNNNNNNNN AAAGGTTGCT GAACATACTG AACACTGAAG GAGCATAGCA ACAAGTAGGA TGTATTTGAA AGTCCATGCT ATTCATAGTT CTTAGCACTG GAGAGTGACC TTGGGTTATC CACATTAAAG GTTCACACAG TTGCCTCCAA CCTCTTACTA CTATTATGAT TAAAAACACT ACCTCTGGCT CATTTATTGA CTCATTTATCA CTCATTTATCA	NNNNNNNNN NNNNNNNNN TTACGAGGAA ACATATTAAT GAGGCTTATG TCTTTTATTT TTATGAGGAA TTATTTTTC ATCCCCCCA GCCTTAGGAT AATCAGAGAG GATGCTGTAC TCGTCTTATT AGCAGATACT CCAGGAAGAG AGCTCAAGGA ATTTGACTCT CCCCTTATT ATTAAAGGTC CCCTTATTT ATTAAAGGTC CCCTTATTT ATTAAAGGTC CCCTATATT AGTGCCTACTA ACCTACCACA GATCAGGAAA	NNNNNNNN NNNNNNNNN GTTAAATTTA TCTTTGAAAA CTTAGGGTTT AGAAGAAAT CCCTGAAAAT TCTTTGGAAA AGCTAAGACT ACATTTATAG AAAACTTGAG AAGAGTAGGT CTCATCACAA GAGATTCAGC GCAGAGGCAG GAGTGAGCTT TAAGATAATC TAAAGACAA GTTCATCCTT AACTCTAGAT TTCCTGTAAG AAACAAACA	NNNNNNNN NNNNNNNN AAAGTAGAAG GAAATTTATA TATGTTAGGA TAATTCTTAA TATATACAAA AGGCATTAT GCTTCTGCTC GGGACCCTCA AGGCATTTGC CTCGAAATGT ATGGTGAAGA AAGTGAGAAA AATCCTCACC TACCCTTCAT CTGAGATTTA ATATGTCTAA TGAATGATAA CAAAGAACAA ATGTTTTTAA GTAGGTATCA AAACAAAAAA	NNNNNNNNN NNNNNNAAA GCAAAGAATT ACTGATATCT GTTTGGTTTA TATGGAATTC GTTTATTTTG TCACCAAAGG ATCCTCAGCG ATCTTAAAAA GAGGTTAAAT GGTACTTTTC AATGGTCAGC ACCTGTCCTG CCACTTCTGT ATTTACTCAT AACCAGAAAA AAATGATTTT AGGGATTGGT AAATAGCCCC TATATGCTAT TTCATTATAC AAACAAGACT
23251 23351 23451 23451 23551 23551 23601 23751 23751 23751 23851 23901 24051 24051 24151 24251 24251 24251 24351 24361	NNNNNNNN NNNNNNNNN AAAGGTTGCT GAACATACTG AACACTGAAG GAGCATAGCA ACAAGTAGGA TGTATTTGAA AGTCCATGCT ATTCATAGTT CTTAGCACTG GAGAGTGACC TTGGGTTATC CACATTAAAG GTTCACACAG TTGCCTCCAA CCTCTTACTA CTATTATGAT TAAAAACACT ACCTCTGGCT CATTTATTGA CTCATTTATTGA CTCATTTATTGA CTCATTTATTGA CTCATTTATTCA TTCTAGGGAA	NNNNNNNN NNNNNNNNN TTACGAGGAA ACATATTATT GAGGCTTATG TCTTTTATTT TTATGAGGAA TTATTTTTC ATCCCCCCA GCCTTAGGAT AATCAGAGAG GATGCTGTAC TCGTCTTATT AGCAGATACT CCAGGAAGAG AGCTCAAGGA ATTTGACTCT CCCTTATTT ATTAAAGGTC CCCTTATTT ATTAAAGGTC CCTATAGTTA GTGCCTACTA ACCTACCACA GATCAGGAAA AGATGCTGAA	NNNNNNNN NNNNNNNNN GTTAAATTTA TCTTTGAAAA CTTAGGGTTT AGAAGAAAT CCCTGAAAAT TCTTTGGAAA AGCTAAGACT ACATTTATAG AAAACTTGAG AAGAGTAGGT CTCATCACAA GAGATTCAGC GCAGAGGCAG GAGTGAGCTT TAAGATAATC GAATGAGAAT ACAAAGCCAG GTTCATCCTT AACTCTAGAT ACTCTAGAT ACTCTAGAT ACTCTAGAT ACTCTAGAT AACCAAAACA	NNNNNNNN NNNNNNNN AAAGTAGAAG GAAATTTATA TATGTTAGGA TAATTCTTAA TATATACAAA AGGCATGTAT GCTTCTGCTC GGGACCCTCA AGGCATTTGC CTCGAAATGT ATGGTGAAGA AAGTGAGAAA AATCCTCACC TACCCTTCAT CTGAGATTTA ATATGTCTAA TGAATGATAA CAAAGAACAA ATGTTTTAA GTAGGTATAA CAAACAAAAAA TCTTCTACAT	NNNNNNNNN NNNNNNAAA GCAAAGAATT ACTGATATCT GTTTGGTTTA TATGGAATTC GTTTATTTTG TCACCAAAGG ATCCTCAGCG ATCTTAAAAA GAGGTTAAAT GGTACTTTC AATGGTCAGC ACCTGTCCTG CCACTTCTGT ATTTACTCAT AACCAGAAAA AAATGATTTT AGGGATTGGT AAATAGCCCC TATATGCTAT TTCATTATAC AAACAAGACT CCATTCCTTT
23251 23351 23451 23451 23551 23551 23601 23751 23751 23851 23951 24901 24051 24251 24251 24251 24251 24451 24451	NNNNNNNN NNNNNNNNN AAAGGTTGCT GAACATACTG AACACTGAAG GAGCATAGCA ACAAGTAGGA TGTATTTGAA AGTCCATGCT ATTCATAGTT CTTAGCACTG GAGAGTGACC TTGGGTTATC CACATTAAAG GTTCACACAG TTGCCTCCAA CCTCTTACTA CTATTATGAT TAAAAACACT ACCTCTGGCT CATTTATTGA CTCATTTAAT CTATTTTAAT CTATTTTAAT CTATTTTTAAT CTATTTTTAAT CTATTTTTACA TTCTAGGGAA CTGAAGATCT	NNNNNNNN NNNNNNNNN TTACGAGGAA ACATATTATT GAGGCTTATG TCTTTTATTT TTATGAGGAA TTATTTTTC ATCCCCCCA GCCTTAGGAT AATCAGAGAG GATGCTGTAC TCGTCTTATT AGCAGATACT CCAGGAAGAG AGCTCAAGGA ATTTGACTCT CCCTTATTT ATTAAAGGTC CCCTATATTT ATTAAAGGTC CCCTATATTT ACCTACCACA GATCAGGAAA AGATGCTGAA TCCTAATATG	NNNNNNNN NNNNNNNNN GTTAAATTTA TCTTTGAAAA CTTAGGGTTT AGAAGAAAT CCCTGAAAAT TCTTTGGAAA AGCTAAGACT ACATTTATAG AAAACTTGAG AAGAGTAGGT CTCATCACAA GAGATTCAGC GCAGAGGCAG GAGTGAGCTT TAAGATAATC GAATGAGAAT ACAAAGCCAG GTTCATCCTT AACTCTAGAT TTCCTGTAAG TAGAACACAT ACAGGTAGGG	NNNNNNNN NNNNNNNN AAAGTAGAAG GAAATTTATA TATGTTAGGA TAATTCTTAA TATATACAAA AGGCATGTAT GCTTCTGCTC GGGACCCTCA AGGCATTTGC CTCGAAATGT ATGGTGAAGA AAGTGAGAAA AATCCTCACC TACCCTTCAT CTGAGATTTA ATATGTCTAA TGAATGATAA CAAAGAACAA AGTGTTTACA AAACCAAAAAA TCTTCTACAT ATTTGTCTTA	NNNNNNNNN NNNNNNAAA GCAAAGAATT ACTGATATCT GTTTGGTTTA TATGGAATTC GTTTATTTTG TCACCAAAGG ATCCTCAGCG ATTTTAAAAA GAGGTTAAAT GGTACTTTC AATGGTCAGC ACCTGTCCTG CCACTTCTGT ATTTACTCAT AACCAGAAAA AAATGATTTT AGGGATTGGT AATAGCCCC TATATGCTAT TTCATTATAC AAACAAGACT CCATTCCTTT AGATTTAAAC
23251 23351 23451 23451 23551 23551 23561 23751 23751 23751 23751 23851 24901 24051 2401 24251 24251 24251 24351 24451 24451 24451	NNNNNNNNN NNNNNNNNN AAAGGTTGCT GAACATACTG AACACTGAAG GAGCATAGCA ACAAGTAGGA TGTATTTGAA AGTCCATGCT ATTCATAGTT CTTAGCACTG GAGAGTGACC TTGGGTTATC CACATTAAAG GTTCACACAG TTGCCTCCAA CCTCTTACTA CTATTATGAT TAAAAACACT ACCTCTGGCT CATTTATTGA CTCATTTAAT CTATTTTACA CTCATTTAAT CTATTTTACA CTCATTTAAT CTATTTTACA CTCATTTAAT CTATTTTACA CTCATCAGGAA CTGAAGGTA	NNNNNNNNN NNNNNNNNN TTACGAGGAA ACATATTAAT GAGGCTTATG TCTTTTATT TTATGAGGAA TTATTTTTC ATCCCCCCA GCCTTAGGAT AATCAGAGAG GATGCTGTAC TCGTCTTATT AGCAGATACT CCAGGAAGAG AGCTCAAGGA ATTTGACTCT CCCTTATTT ATTAAAGGTC CCTATAGTTA GTGCCTACTA GTGCCTACAC ACCTACACA ACATCAGGAAA ACATCAGGAAA TCCTACATAT TGAAGAGACA	NNNNNNNN NNNNNNNNN GTTAAATTTA TCTTTGAAAA CTTAGGGTTT AGAAGAAAT CCCTGAAAAT TCTTTGGAAA AGCTAAGACT ACATTTATGAG AAAACTTGAG AAAACTTGAG AAGAGTAGGT CTCATCACAA GAGTTCAGC GCAGAGGCAG GAGTGAGCTT TAAGATAATC GAATGAGAAT ACAAAGCCAG GTTCATCCTT AACTCTAGAT TTCCTGTAAG AAACAAAACA	NNNNNNNN NNNNNNNN AAAGTAGAAG GAAATTTATA TATGTTAGGA TAATTCTTAA TATATACAAA AGGCATGTAT GCTTCTGCTC GGGACCCTCA AGGCATTTGC CTCGAAATGT ATGGTGAAGA AAGTGAGAAA AATCCTCACC TACCCTTCAT CTGAGATTTA ATATGTCTAA TGAATGATAA CAAAGAACAA ATGTTTTAA GTAGGTATCA AAACAAAAAA ATCTTCTACAT ATTGTCTTAC	NNNNNNNNN NNNNNNAAA GCAAAGAATT ACTGATATCT GTTTGGTTTA TATGGAATTC GTTTATTTTG TCACCAAAGG ATCCTCAGCG ATTTTAAAAA GAGGTTAAAT GGTACTTTTC AATGGTCAGC ACCTGTCCTG CCACTTCTGT ATTTACTCAT AACCAGAAAA AAATGATTTT AGGGATTGGT AAATAGCCCC TATATGCTAT TTCATTATAC AAACAAGACT CCATTCCTTT AGATTTAAC AACCAGAGACT
23251 23351 23451 23451 23551 23551 23601 23751 23751 23751 23751 23751 24001 24051 2401 24251 24201 24251 24351 24351 24451 24551	NNNNNNNN NNNNNNNNN AAAGGTTGCT GAACATACTG AACACTGAAG GAGCATAGCA ACAAGTAGGA TGTATTTGAA AGTCCATGCT ATTCATAGTT CTTAGCACTG GAGAGTGACC TTGGGTTATC CACATTAAAG GTTCACACAG TTGCCTCCAA CCTCTTACTA CTATTATGAT TAAAAACACT ACCTCTGGCT CATTTATTGA CTCATTTAAA CTCATTTAAA CTCATTTAAA CTCATTTAAA CTCATTTTACA TCTATGGGAA CTCAAGGTA AACTGGAAA	NNNNNNNNN NNNNNNNNN TTACGAGGAA ACATATTAAT GAGGCTTATG TCTTTTATT TTATGAGGAA TTATTTTTC ATCCCCCCA GCCTTAGGAT AATCAGAGAG GATGCTGTAC TCGTCTTATT AGCAGATACT CCAGGAAGAG AGCTCAAGGA ATTTGACTCT CCCCTTATTT ATTAAAGGTC CCCTATATT ATTAAAGGTC CCTATAGTTA GTGCCTACAC GATCAGGAAA AGATCAGGAAA AGATCAGAAA AGATGCTGAA TCGAGAGACA GGAGACAGAG GGAGACAGAG	NNNNNNNN NNNNNNNNN GTTAAATTTA TCTTTGAAAA CTTAGGGTTT AGAAGAAAT TCTTTGGAAA AGCTAAGACT ACATTTATAG AAAACTTGAG AAAACTTGAG GAGAGGCAG GAGTGAGCTT TAAGATAATC GAATGAGAAT ACAAGCCAG GTTCATCCTT AACTCTAGAT TTCCTGTAAG AAACAAACA TACAAACAA AACAAACA TACAGACAGG GGCAGAAGAG AACAAACAA	NNNNNNNN NNNNNNNN AAAGTAGAAG GAAATTTATA TATGTTAGGA TAATTCTTAA TATATACAAA AGGCATGTAT GCTTCTGCTC GGGACCCTCA AGGCATTTGC CTCGAAATGT ATGGTGAAGA AAGTGAGAAA AATCCTCACC TACCCTTCAT CTGAGATTTA ATATGTCTAA TGAATGATAA CAAAGAACAA ATGTTTTAA GTAGGTATCA AAACAAAAAA TCTTCTACTTA CTTCACTATC AACATAACTG	NNNNNNNNN NNNNNNAAA GCAAAGAATT ACTGATATCT GTTTGGTTTA TATGGAATTC GTTTATTTTG TCACCAAAGG ATCCTCAGCG ATTTTAAAAA GAGGTTAAAT GGTACTTTTC AATGGTCAGC ACCTGTCCTG CCACTTCTGT ATTTACTCAT AACCAGAAAA AAATGATTTT AGGGATTGGT AAATAGCCCC TATATGCTAT TTCATTATAC AAACAAGACT CCATTCCTTT AGACTTGCAG AACTTGCAG AACTTGCAG AACTTGCAG AACTTGCAG AACTTGCAG AACTTGCAG
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23251 23351 23451 23451 23551 23551 23601 23651 23751 23751 23751 23851 23951 24051 24051 24201 24251 24301 24351 24451 24551 24651	NNNNNNNN NNNNNNNNN AAAGGTTGCT GAACATACTG AACACTGAAG GAGCATAGCA ACAAGTAGGA TGTATTTGAA AGTCCATGCT ATTCATAGTT CTTAGCACTG GAGAGTGACC TTGGCTTCAA CTCTTACTA CTATTATGAT TAAAAACACT ACCTCTGGCT CATTTATGA CTCATTTATCA CTATTTATCA CTATTTATCA CTATTTTACA TCTATGAGGAA CTCACAGGTA AAACTGGAAA TTCTAGGAAA TTCTAGGAAA TTCTAGAAGGCAAA	NNNNNNNNN NNNNNNNNN TTACGAGGAA ACATATTAAT GAGGCTTATG TCTTTTATT TTATGAGGAA TTATTTTTC ATCCCCCCA GCCTTAGGAT AATCAGAGAG GATGCTGTATT AGCAGATACT CCAGGAAGAG AGCTCAAGGA ATTTGACTCT CCCTTATTT ATTAAAGGTC CCTATAGTTA GTGCCTACTA ACCTACCACA GATCAGGAAA AGATCAGAAA TCCTACTA GTGCCTACTA GTGCCTACTA GTGCCTACTA ACCTACCACA GATCAGGAAA AGATCACACA GATCAGGAAA AGATCAGAAG TCGAAGAGACA GGAAGGTGAG GGAAGTGAG GGAAGTTGGCA	NNNNNNNN NNNNNNNNN GTTAAATTTA TCTTTGAAAA CTTAGGGTTT AGAAGAAAT TCTTTGGAAA AGCTAAGACT ACATTTATAG AAAACTTGAG AAAACTTGAG AAGAGTAGGT CTCATCACAA GAGATTCAGC GCAGAGGCAG GAGTGAGCTT TAAGATAATC GAATGAGAAT ACAAAGCCAG GTTCATCCTT AACTCTAGAT TTCCTGTAAG AAACAAAACA	NNNNNNNN NNNNNNNN AAAGTAGAAG GAAATTTATA TATGTTAGGA TAATTCTTAA TATATACAAA AGGCATGTAT GCTTCTGCTC GGGACCCTCA AGGCATTTGC CTCGAAATGT ATGGTGAAGA AAGTGAGAAA AATCCTCACC TACCCTTCAT CTGAGATTTA ATATGTCTAA TGAATGATAA CAAAGAACAA ATGTTTTAA GTAGGTATCA AAACAAAAAA TCTTCTACTT ATTGTCTTAC AAACAAAAAA TCTTCACTTAC AACATAACTG ACCCATGCCG CCTCTAGAGC	NNNNNNNNN NNNNNNAAA GCAAAGAATT ACTGATATCT GTTTGGTTTA TATGGAATTC GTTTATTTTG TCACCAAAGG ATCCTCAGCG ATTTTAAAAA GAGGTTAAAT GGTACTTTTC AATGGTCAGC ACCTGTCCTG CCACTTCTGT ATTTACTCAT AACCAGAAAA AAATGATTTT AGGGATTGGT AAATAGCCCC TATATGCTAT TTCATTATAC AAACAAGACT CCATTCTTT AGATTTAAAC AACGTTGCAG AGTCCTAAGC TAGAACCCTC TAGAACCCTC TAGAGGTGAA
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23251 23351 23451 23451 23551 23551 23651 23751 23751 23851 23751 23851 23951 24001 24151 24201 24251 24201 24251 2451 2451 2451 2451 2451 2451 24	NNNNNNNN NNNNNNNNN AAAGGTTGCT GAACATACTG AACACTGAAG GAGCATAGCA ACAAGTAGGA TGTATTTGAA AGTCCATGCT ATTCATAGTT CTTAGCACTG GAGAGTGACC TTGGCTTCAA CTCTTACTA CTATTATGAT TAAAAACACT ACCTCTGGCT CATTTATGA CTCATTTATCA CTATTTATCA CTATTTATCA CTATTTTACA TCTATGAGGAA CTCACAGGTA AAACTGGAAA TTCTAGGAAA TTCTAGGAAA TTCTAGAAGGCAAA	NNNNNNNNN NNNNNNNNN TTACGAGGAA ACATATTAAT GAGGCTTATG TCTTTTATT TTATGAGGAA TTATTTTTC ATCCCCCCA GCCTTAGGAT AATCAGAGAG GATGCTGTAC TCGTCTTATT AGCAGATACT CCAGGAAGAG AGCTCAAGGA ATTTGACTCT CCCTTATTT ATTAAAGGTC CCTATAGTTA GTGCCTACTA ACCTACCACA GATCAGGAAA AGATCACACA GATCAGGAAA TCCTAATGTTA TGAAGAGACA GGAAGGTGAG GGAAGTGGCA TAAAGTAAAT	NNNNNNNN NNNNNNNNN GTTAAATTTA TCTTTGAAAA CTTAGGGTTT AGAAGAAAT TCTTTGGAAA AGCTAAGACT ACATTTATAG AAAACTTAGG AAAACTTAGG AAGAGTAGGCAG GCAGAGGCAG GAGTGAGCTT TAAGATAATC GAATGAGAAT ACAAAGCCAG GTTCATCCTT AACTCTAGAT TTCCTGTAAG AACAAACA TAGAACACAT ACAGGTAGGG GGCAGAAGAG AACTAGAAGC CTGTCATGTG GACATTGTTT	NNNNNNNN NNNNNNNN AAAGTAGAAG GAAATTTATA TATGTTAGGA TAATTCTTAA TATATACAAA AGGCATGTAT GCTTCTGCTC GGGACCCTCA AGGCATTTGC CTCGAAATGT ATGGTGAAGA AAGTGAGAAA AATCCTCACC TACCCTTCAT CTGAGATTTA ATATGTCTAA TGAATGATAA CAAAGAACAA ATGTTTTAA GTAGGTATCA AAACAAAAAA TCTTCACTTA CTTCACTTA CTTCACTTA CTTCACTTA CTTCACTTA CTTCACTTA CTTCACTTA CTTCACTTACTA CACATAACTG ACCCATGCCG CCCTTGAGCC GGATATCTAT	NNNNNNNNN NNNNNNAAA GCAAAGAATT ACTGATATCT GTTTGGTTTA TATGGAATTC GTTTATTTTG TCACCAAAGG ATCCTCAGCG ATTTTAAAAA GAGGTTAAAT GGTACTTTTC AATGGTCAGC ACCTGTCCTG CCACTTCTGT ATTTACTCAT AACCAGAAAA AAATGATTTT AGGGATTGGT AAATAGCCCC TATATGCTAT TTCATTATAC AACAAGACT CCATTCCTTT AGATTTAAAC AACGTTGCAG AGCTCTAAGC TAGAACCCTC TAGAAGCTCC TAGAAGCTCC TAGAAGCTCC TAGAAGCTCC TAGAAGCTCC TAGAAGCTCC TAGAAGCTCC TAGAAGCTCC TAGAAGCTCC TAGAAGCTCC TAGAAGCTCC

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PENNI TOTOCACATT TIGACCAATC CAAGAAGGAA GAIIIAAAAI IAICAACAII
PENEL CONCATTITO TANTICANCA TOCAGGOCCAC AGGLAGAAGG AACACIAIAG
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- 10751 CCCACATTCT CCCATTCCAC 1161A( )((A GCC1GGGCAA CAAGA)
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- SOUTH AACCTAATTC ATCTGGTAAC AALAGCAALA ACALAAALAG CAGIAAIAG
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30101 GTAATAATCT CCTCTAGGAT GCTTTGCTGG ATTTCCCTGG ACTAGGTTGT
30101 GTAATAATCT CCTCTAGGAT CTCCCTACGG CAGCACTGCT 30151 CTTTTCCTGC TACTTTCTCC CATTACAGGT CTCCCTACGG CAGCACTGCT
20201 TATATCACTT CCAACTTGAA 1(141111111 1888888888 9110000011
TABLE TARACTERS AND
20201 CTATATTCTT ATACACCCAG GCACATTAAI GCCAICAGCI IIAGCCCIII
20251 ATCTTCTCAT TTTACTTTAT TCCAAAIGIC AGCIIIAICC IGIIGGAIGI
20401 CCTCATCTTT TTTCTCTACA TTCAGCCAGI ICCAIICICA IGIICIGGAA
20451 CCTTCTCACA CACCCCCAAT ATGCATIICA AGAICAGAAG AICCAGAGIG
20E01 AAAATCATTG GAATGGCCTG AGTCACAGII CCAATCCIAG AACAAGGCAI
PAREL CTTCCTACCC ATCTCAGAGA TGATAAGIGA CAGAIACAGI GACAGCAAGI
PAGE COTTONTOGO ATOTONOTTO TGAGAGAGGG ICIGIGAAAA AIGAAAGACC
PACEL TOCATARCAR CACCAGAGAGC AGAAATATGA ACALIGIIGI GAGICAGGIC
20701 TITACCCAAC TCTCTCCTCC TTATTCTACL IIIIIGIGGA AGAIIGAIIA
20751 TCTCTCTTTA ATAGAATGCA GTAAAGAACA GIGIIGGAGG GCAGCIGIGG
20001 ACTCCACTTC ACTCCCACTC TACCACTCIG CLACITACL ACTIVITION
ACCEL CTTCACAAAC CTACTTAATT TCCCTGGGII GLAGIIIGII CACCIAAAA
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30951 TATATGTAAC ATATTTAGAA TAATGATGGG TATTCCTTAT GTAAATGTTA
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21001					
2 TOOT	GATGTTAGCT	ACTGTGAATT	TTTCTGTTGT	TCCACTAGAC	TGTAGGACCC
31051	CTGAAGGCAG	CCAACCTTCC	CCTTCTTTCT	CCCACCACCT	ACCACAATCC
	CTOAMOGCAG	GCAACCTIGG	GCTTCTTTCT	CCCAGCACCI	AGCACAATGG
31101	CIGITACTIA	GTAAGCAGTC	<b>AGTAATGGTG</b>	TGTTGTTGTC	AGTGAACACA
31151	GACTGAGTTC	AGTGAGCAAT	<b>GTCTTGGAAA</b>	GCCTCTACTG	CACCTAGGAC
31201	TTTCAGCTAT	ACTGAGACAG	AAAAATGAAA	TOCTOTOTO	ACTCCAAACC
	ACAACCCAA	ACTORGACAG	AAAAATGAAA	ICCICICIO	ACTGGAAAGC
31251	AGAAGCCAGA	CATGTAGGCA	ACCAAACTGT	AACTGTTTCC	ATGTCGAATT
31301	GACTTTGCCT	TTAGCGAATC	ATAGCACTGA	GGAGTGTCAC	GTTTAAGCAG
31351	CANATTTETA	TAGCAAATTA	ACATGCCAAA	AAACCCATCC	AACACTTTTA
	COANTITUTA	TAGCAAATTA	ACATOCCAAA	AAAGGCATGC	
31401	CHGAIIII	HCCCCTCCT	CTCTGGGGAA	TITATCTTAT	TTGGGTCTTA
31451	TCTTGGAATT	TATCTTATCT	TGAACTTATT	CAGACTGCAT	TGGTTTAATT
31501	TGCTATCAAC	TGGGGCTATA	<b>TAGTGCACTG</b>	CAATTTAATC	TCTTCTATAT
31551		TACCAAATAA	CCACATAACC	AACATATOO	IGITGIAIAI
	GIGAAATATI	TACCAAATAA	CCACATAACC	AAGATATGGA	GGACCTACTT
31601	TAAGAGGAGA	TTCTTGCAAA	<b>GCACCTTAAA</b>	AGCATACACT	CAATAATCAC
31651	AATGGCATGA	CTGCATACAG	<b>GGAGATAATC</b>	AGTTGTTTTA	ACTITIONT
31701	TAACCACTAC	CACAATCACT	TTTTCCCAAC	TTACCAATTT	CCAAACCTTT
	TAAGCAGTAG	CAGAATGACT	TTTTGGGAAC	ITAGGAATTI	GGAAACCIII
31751	TTATTCTATG	TATTGAATAT	CAACTATGTA	ATTTAGTCTA	AGGTTATATG
31801	CTAGAAACAT	TTCAAAAACG	AAAGCAGCAG	CAATGACATC	ΔΑΔΔΔΤΓ
31851	GTCAAAAGCA	AATGGTTTTA	AATAGAAATA	CATCATTTA	ACAATCTTCA
	ACTITAAAA	ATCCTATAAA	AATAGAAATA	CATCATTTA	ACAATCTIGA
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31951	AGATTGATAC	ATTTAACTAC	ATAAAATTTA	AAACTACATT	ACTGAAAAA
32001	AATCTGAGAC	<b>AGGGTCTCTG</b>	TCACCCAGGC	TECCETTECAC	TEGTECEATE
22051	ACACCTTACT	CCACCCTTCA	CTTCCCACCC	TTALCCCTC	TOUTUCGATC
3203T	ACAGCTTACT	GCAGCCTTGA	CTTCCCAGGC	TTAAGGGCTC	AIGIAAICCI
32101	CCCATCTTAG	CCTCCCAAGT	AGATGGGACC	ACAGGCATGC	ATCACCACAC
32151	<b>TCGACTAATG</b>	TTTAATTTT	TTGTTGTTGA	GACAGTCTCC	CTATGTTGCT
	CAGGCTGGTC		CCCCTCAACT	CATTCTCCTC	CCTCACCCTC
32201	TCAAACTCCT	ICIAACICCI	GGGCTCAAGT	GATICICCIG	CCTCAGCCTC
32251		AGAATTACAG	GTATGAACCA	CTGAGCCTGG	CTTTAAAAGT
32301	TTTTAAAATC	AAAAGCCAAA	TGGACAACCT	AGAAAAAATA	CTCCTGAGAT
32351	ATGTTAAACA	GAGTTAATTT	ACTTGCCATT	TTTAACTCTC	CTTACATATC
22401	AAAAAATCTA	ATAACTCATT	ACTIGCCATI	TITAMOTOTO	CHACATATC
32401	AAAAAATCTA	ATAACTCATT	AAAGATATGT	AAAAIAIAIA	CAAAGGCAGT
32451	TTGCTGAAAA	AATACACATA	TAAATATATG	CAGCTTCACT	CAGCATTCAA
32501	GAAATAAAGT	ΑΔΑΤΟΔΔΤΔΔ	TTCAATCTTT	TTCACTTGTC	AGATGAAGAA
	CAGTTAATGT	ACTACTCTTC	CCAACCTCCT	CCACAAAAAC	TTATETTAT
32331	ATCTTTTCA	AGIAGIGIIG	GCAAGGTGGT	GGACAAAAAG	HALLITAL
3200T	ATGTTTTTGA	TATCAAGAAG	ATTTGATGCA	ACATCTTTGA	AGAGCCAGTT
32651	<b>AATAATATCT</b>	GTAAAATTAG	AAAATTAACA	TATTCTTTGC	CCAGCATTTC
32701	TACTITITATO	AACTITECTT	GTAAACAGAC	ACACAACCCC	ATCAACAATC
32751	CTCAAGGTAG			TITITITI	TTTTGACGGT
32801	<b>GTCTTGCTCT</b>	GTCACCCAGG	CTGGAGTGCA	ATGGCACAAT	CTTGGCTCAC
32851	TGCAATGTCC	<b>GCCTCCTGGG</b>	TTCAACCCTC		
32901				TTGCAGGAAG	
	$C \wedge \wedge \wedge C C C \wedge C C$	CACTCCCTAA	AACCATCCCA	TTGCAGGAAG	TCAGGGACCC
32951	CAAACGGAGG	GACTGGCTAA	AACCATGGCA	GAAGAACATG	TCAGGGACCC
3-33-	CAAACGGAGG ATTTCATGGA	GACTGGCTAA	AACCATGGCA ATCCCCCAAA	GAAGAACATG	TCAGGGACCC GACTGTGAAG
33001	ATTTCATGGA	GACTGGCTAA CATTTATTAG	AACCATGGCA ATCCCCCAAA	GAAGAACATG TTAATACTTT	TCAGGGACCC GACTGTGAAG TATAATTTCT
33001	ATTTCATGGA TATGCCTGTC	GACTGGCTAA CATTTATTAG TTTACTGCAA	AACCATGGCA ATCCCCCAAA TCTCTGANNN	GAAGAACATG TTAATACTTT NNNNNNNNN	TCAGGGACCC GACTGTGAAG TATAATTTCT NNNNNNNNN
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34101 TGGCCAGGGT GGTCTCAAAC TCCTGACCTC TGGTCATCCA CCCGCCTCAG
24161 CCTCCCAAAC TCCTCCCATT ALAGGGGGTA GCCACTGCAC TCAGCACTG
24204 CACATAATTA AACCATCIII (QQQQI((QI (QAIAAQIID CC!C!!!!
24251 CCTACATTTA CACAATAAAA IACAAAIIAG CIACIIAAAA AIAAIIAAA
24201 CTATATCTCA TCCTATGAAT GGALAGGGL AAIGIGIIAI ACAGAGGG
AARSAACAATC TATCCTCCCA TIGGAAIGAI AGIAIGIIGG IMIIGGIGG
24401 ACCAACCACT ACATATATCC AGAGAGAAL ILLIAAAGGG IACACAACCA
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SAFO1 CAACATACCT TACTTITCAC IGAALAALIG IIGIAGIIAA AAAAAAAAAAAAAAAAA
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34601 TOATCTTCAA ACTCACCTCA CTTAGGIIIA AIIAGGICCA IIIIACAGAC
24CE1 ACACACATTC TTATTTGAAA GALLGAGIAA CIAGICIAAG GIIACACAC
34304 -cc+c+c+c+c CTTCCTTCT1 (AG1AGAGG G111ACATAA ACAGCAAGG
34001 CCTCCAATCA ATTITTAGAA AAAAIAAAAI CIIIIQCAAA QATTITTAGAA AAAAIAAAAI CIIIIQCAAA QATTITTAGAA
- 3 4 0 E 4 - + C A A A A T A C - A A A A A A A A A A A A A A A A A
- 3 4001 CTCTC 4 A ATT CC 8 8 CC 8 TC A GGG [G] [G] A A A A A CAGACICIA AAAAAAAA A GGG [G] [G] A A A A A A A A
- 2 4 CE 4 COMPONITO TO CONTINUO ATTIGITATA GLACIALI GLACAGLATA TIVAVA CAVA
SEANS SARCETA ACTOMATAN ANIMADISTAD BIBBBBBB ICHICHCICO
APARA ATTECAÇAAT CACCATECIT LAIG LAAGG GAAAGACILO UMMACELIO
36161 TOTOATTOTA COTTTGGGAI (4641A641A1 GIIAIACAA) AAAAAAAA
SESES CALACCTCCA TATTCAATTT ACCTGAGIGG AALIAGGLAG ACICAAGIGA
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- 55564 666646464 AACCACATAG AALIGUUUL UU
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35701 TGAGCCTGAG TACCCTCAGA TGTACTGACC ACCCTCATAA ACAGATCCCT 35751 AGTGACATAA AAATGAAACA TGTACTGACC ACCCTCATAA ACAGATCCCT
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35851 CACCCAAAAG AAAAACTCTG AAATAAGTAC TTTGTGTGTGT 35901 AATATTCCAA GTAATTATCA CAACATTAAG GTGCATTCAG CTTTGTGTGT
35901 AATATICCAA GIAATIATCA CAACATITAG GATACTGTAC AGATACAATG 35951 TAACGTGGTA TACCTCCAGG CAACTTTAG GATACTGTAC AGATACAATG
ACAAL ACTOTOLAGO OTCOCATOLA ALGANICACIÓN CIGARICAGUA CIUAGUCACI
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- 56464 64-4666-46 6666-6666-6666-6666-6
ACARA TOCOCOACACT AAACCACTAC ( )   AAAAAAAA CACACACACACACACACACACACACACA
SCOOL AACCETAACT TTCCTTTACA GGIIAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
~~~~~ ^~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
- 564F4 66-4-7-7-66-7 66-6-8-6-7-10-10-10-10-10-10-10-10-10-10-10-10-10-
ACEDA TAAAACCACT TACTTCCACC (AAIAIII IA IGCACAIGAC CCCIII CCCI
- 665546ATAAA CCTCATCAAC AAIAIAILAI LIILAICULU AIIIIAAA
ACCOS -COLCALACO CALOCOATACA (GIADAIIII LAAGAIIAUA CAUCIAIII)
~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~
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\$6654 \$46464TTCC \$4CTCCACT!
34454 CTCAACATT TAAAAACCCA ( )GIGGA
37101 GTTGAACATT TAAAAAGGGA CTGTCAGGAA CCTGTTGCCC AGGCTGGTGT 37151 AGTCACTTTT TTTTTTGAGA AAGGATCTCA CCTGTTGCCC AGGCTGGTGT

37201	GCAGTGGTGC	AATCACAGAT	AACTGCAGCC	TCAACCTCTT	AGGTTCAAGT
37251	TCCCCCTGCC	TCAATTTCTG	AGTAGCTGGG	ACTACAGATG	TGCACCACCA
37301	TOCCTACCAA	ATTITTAATT	TTTTCTACAC	ATCCCCCCTC	ACTACATTAC
	TOCCTAGCAA	ATTITIAATT	TTTTGTAGAG	AIGGGGCCIC	ACTACATTAC
3/32T	CCAAGCTAGT	CTTGAACTCC	TGGGCTCAAG	CAATGCTCCT	GCCTCGGCCT
37401	CCCAAAGTGC	TGGGATTACA	GGTGTGAGTG	ACTGCATCCA	GCCTCTTATA
37451	<b>GTCACTTTTA</b>	ATCTATCATT	GGCTTTCCCA	TTAGATTCTA	CTCTTATACA
37501	ACCAACTCAC	TTCACACACT	ATCCCACTAC	ACTACACCCT	CIGITATACA
3/301	AGGAAGTGAC	TICAGACAGI	ATGGCACTAG	ACTAGAGGCT	GIGITITICT
3/22T	TTAATAAAGG	CATAAATGAG	ATGAATTGCT	CTAAGGCTTT	AGGCTTGTCC
37601	CTTTTCTGAG	AAGTGACCTT	TGGGAGGTCA	CATTTAGTTA	AAGCAGTTTT
37651	<b>GCTAGTATAA</b>	ATTTACCAGG	ATCCTGACAT	GTAATCCTGT	ATCATTTTCA
37701	CTAACCTTAA	AATCCTATAT	CAAACCACCT	CCTTCACCAA	ATCCATTALT
37701	GTAAGGTTAA	AAIGGIAIAI	GAAAGGAGGI	GGTTCACGAA	AIGGAIIAAI
3//51	ATCAACATGG	AACTTCATGC	TTTCTAGGTA	CCTGCTGCAT	CCTTGGAGAT
37801	TCAAAATGTC	ATCATGGCAT	TCTAGGCTAG	ACTGGCAGTG	GAGAAATCAC
37851	TGTGAGTTAT	TGGATTTGCT	CAAGATAAAA	TCTTGAATTT	CCAAATAAAT
37901	CCTGGTCAGC	TTTTTAAC	ACTCTTCTCC	TAAATAATAC	ACAACTCACA
37001	CCIGGICAGC	TITITIAAC	ACICITOTO	TAAATAATAC	ACAACTCAGA
3/337	TTCATGTAAT	GGGTGTAAGA	AAATCATIGC	HIGGHAIT	TCAGTATGAA
3800T	ACTCAAGAGA	AAACTTACTG	AAGTGTTTTT	AAAATTATTC	TGACCACAAC
38051	CCAAGGTAAA	ACATAAGCCA	AAAAACATAT	CATGACATAG	TAAATGAAGC
38101	CAGGATTGTA	TATATATGTC	TACTCAAGTA	TATGAAATGG	ΔΔΔCΔΔCΔGT
38151	TTCAGAGGCA	GTACTATGCT	TACTACATTT	GAGGCATTTC	TCCTATTTTC
38201	TATTCTATTT	AATTAAATTT	TTACTACTTC	TTATTTACC	TACATTE
30201	TCATALCTCA	AATTAAATTT	TIAGIACTIC	TIATTITAGC	TACATTTATT
2072T	TCATAACTCA	TTAATGGGTT	TTGACTCACA	GCTCAAAAAC	ACTGCCTTAG
38301	AGAATCCAAA	TGTTCACACT	ATCCATATTT	ATAAGAAGTA	ATTGTTCTGG
38351	GGTTCTTGTG	TATTCTTATA	GCTTAGTTTG	ATTTATTTGC	TAAGACCTGG
38401	CTAAGTGAGA	ACTGCAAAGA	GTTATGCCTT	CAACTACCTA	AGCCAGGAAT
38451	TTTCTGAGGT	GGCAGGGGAA	CCAGGGTGAG	CAGAAGGACA	TATCATCCCC
38501	ACCCTCATTA	ACCTTATCCT	ATACTCCATC	AAATAAACTC	ACAACTCAAC
3030I	CACTTTCACA	AGCTIATGCT	ATAGIGGAIG	AAATAAACTC	AGAAGTCAAG
3022T	GAGTTTCAGA	AGAGAAG I CA	TICCCTIGAG	TAACTATGTT	AAGTACGTAA
3860T	ACAGCTTTAG	TAGTGCTTTC	TTAGTACAAG	GTGTTTTCTT	CTGATCTAGG
38651	AGAGTCAGTC	CAATTTTTTT	CTTTTGAGAA	AATGGAGGCT	CAAAGAGTCT
38701	GTCATTTATC	TCCAGTCTCT	TCATTATTTT	GAGTCCAAGT	ACAGGATTAT
38751	TTGTAATATA	CATGCTGCCT	CACATGACTA	ACTCCCTTTT	CTCATACAAA
38801	CCCAATTTCC	ACTTCACAAC	ACAAACTCAT	CATTAACTCA	CATCATTA
30001	GGGAATTTGG	AGTIGAGAAG	AGAAAGIGAI	GATTAAGTCA	CATCATTAAA
3003T	ATGTTTGACT	CICAGATATC	TIGGAAAGAC	TTTGAAGGCA	CTCTAGCCAA
3890T	ACTTTTTCCT	TCAGAAGGAG	CTTATCTAAT	TATTCTAGAT	AATAGAGAAA
38951	<b>AACTAGGTCT</b>	TTTAAAGAGA	CAAATTATAT	ACCATTTAGT	GTTTCACAAT
39001	ATTTTCTGAA	TAAACTTAAA	ATCCCTTATT	TGGAATTTAA	CTCATCTAAA
39051	TCCTTATTTC	AAAAACCAGG	AAACAGAGTC	AAACATTITC	TCACTTATCA
30101	ACCCACTAAA	CCAAACATTC	TCACCTCCAC	AGGAGATET	ATCATTACA
33101	AGGCAGTAAA	CCAAAGATTG	TCACCTGCAC	AGGAGAATCI	AIGAIIIGII
23T2T	CTTCTCATCA	HATACATTI	CACGAGCATT	GACTCAAAAA	ACCATGCTAC
3920T	CTATAAACTA	ATCAACAATT	GCTTCTTCTA	GGGACTGAAA	TTTTAAAATT
39251	TCAGACGTGG	AGGATCGACT	CTACTTCAAA	GCAAAATTCA	GTGGACTTCT
39301	<b>GCACACATAT</b>	CCATTCTAAT	CTGTTACAAG	TCTGCACTTT	GGAGATTAGT
39351	TCATGCTACA	CACTTAGAGG	TCTAATATTT	TCCTACTTCC	CAAAATTCAA
30401	ATTACTTAGA	TACAAAACAC	TCCTTCTACT	AACAAAATAG	GAAAATTGAA
20451	CATTETALAGA	TACAAAAGAG	IGGIIGIAGI	AAGAAAATAG	GCAAGGAGAA
39431	CATTTTAAAG	IGCIGATCCI	CGGTAAAGCC	ATACATAGGA	TGCACCTGGG
3920T	AGCAGATCTT	TCTGAAGTCA	TTCTGTGCTC	AGAGATGTTT	CTCCTTACCT
39551	TGCTGCCTAT	GTCAAATTCT	CTGTGATATG	TTCTTAGAGC	CCCATGACCT
39601	CTCTTCTTAA	CTTGCAGTGG	GAGCTTGAAT	TTTCCATTTA	TTTTTGTGAC
39651	CATTTAGTCT	ATAAGAGTCT	CCGTCTTTAC	AGGGCCCTCA	CCTGACTACA
39701	GACTCCATAA	ACCCACACAT	TCTATTTTTA	CTCTATTATT	ACTCTATTCC
20751	CACCACTAAC	CACTACCATT	ALTACATACT	CICIATIATI	ACIGIATICC
39/31	CAGCACTAAG	CACTAGGATT	AATACATAGT	AAGTGTTCAA	CAGATGTTTA
3980T	CTGGATGATT	AGATTGGCAT	TTTAAGGTAG	TCTGAGATCA	CGTTTTTAGAC
39851	AAGATACTTC	AGTTTAGTCC	AATCTTTATT	ATTTATTAGC	TACTAAAGAG
39901	AAATTGATAA	TTACTCATGA	TATTCTTCTT	TTTTGTTTTA	CAGTCAACTT
39951	TGACCACTTT	GAAATTTTGC	GAGCCATTEC	GAAAGGCAGT	TTTGGGAAGG
40001	TGAGAACAAA	TTCAAATCAT	TAACCACCAC	CACCCTTATC	TACCCCACCC
4000T	44C4C4CC	CCACAAATGAT	TCACCACCAG	CAGGGTTATG	DODADOLCAGG
4000T	AACAGAGGGT	CCAGAAATGT	ICACATTATT	GAGTTGCTGG	GACCACAAGG
40101	AAAGATAATT	AAGTGAAAAT	GTTTTTGTAA	TGGATTTTTA	TAAAATTGTC
40151			TOTOLOGO	ACCTACATAA	TC
	ACCACAGTTT	AAGAAAAGCG	1 G 1 GACAGGC	AGCIACAIAA	IGAACATATA
40201	ACCACAGTTT CTGTTGTCAG	AAGAAAAGCG AATAATCTCA	TTAAACTCAA	ATCTGTTTAC	TCTCAGTAAA
40201	ACCACAGTTT CTGTTGTCAG CTTTAAGGCT	AATAATCTCA	TTAAACTCAA	ATCTGTTTAC	TCTCAGTAAA

40301 TITCAGATTC TACCAGCTGT ATGCCCAGTA ATAGTTATCT TGTTTATGGA
ADREL ACACTTACTT ATTITCATGT GGGAAAGAAG TCATCCGALL ICLALLIGH
ANANI TECTENTITE TETANTETIT TTATETTANG ANANALALAI ALILAGILIA
ANASI ATTITITE CAAGAACTT CTGTATTCAA ACCCIGAIIA CIAGIIICIC
ANSOL ANTOGRACO TACTITAAGA GAATAATATT TCATALAAAA CIIGCAIIII
ACEL AAAATCATTT TCTGTTTACT TTTTCAGGCA TTATACAGAC CICIAAAGAA
40601 ATTTCAAAAA CATGGACATC ATATTTAGTG TTTTTCCAGT CCTTAAAGTC
40651 CTITTTGGTT ATATCATGTA TGGGTTGTAA ACAGAAATTC TTTGCACAGT
40701 ATTATTCAGC TTGACAGTTC AGTCATGTCT ATTTCAGTCA CTCAAAGCAG
40701 ATTATICAGE TIGACAGTTE AGREGATAT TCCTGACATG GAGGCAGCTA
40/51 GATTAGGAT GITACTIGIT ATTIGGATAT TECTAGATA CCAGGCAAAA 40801 TTTTCACCAA AATGCTGTCT TAAAAGCCCA AAAAGCAATA CCAGGCAAAA
40801 TITTCACCAA AAIGCTGCT TAAAAGCCA AAACGCATTCA AACTGCTGCA TAGAAAAGAA
40851 TTGTTTGAGA AAAAAGAGAT CCAAGAATTG AACTGGTGCA TAGAAAAGAA
40901 AATGAAATTT TTAATCTAAA ATCAGAGCTA AGTGGGAGCT TTTAACATCA
40951 TATAATTTGC AAATGTTAAG GATCCAAGCC ACAGCAAAGA ACATGTCTTG
41001 TTCTGTCTCT CATCACCATG ATCCATTATC TCCCTAATCA CTCTCTCACT
41051 CGGGTTTTCA CCATTAGGTC TGCATTGTAC AGAAGAATGA TACCAAGAAG
41101 ATGTACGCAA TGAAGTACAT GAATAAACAA AAGTGCGTGG AGCGCAATGA
A1151 ACTGAGAAAT GTCTTCAAGG AACTCCAGAT CATGCAGGGI CIGGAGCACC
A1201 CTCTCCTCCT TAATTTGTGG TGAGTAATTT TACTGGACCT CTGAATAGAG
A1251 ACACTCCTGT TATCGGTGGG CTAGGGGAGG TCCCCAAAIG CCICIGGGAC
A1301 CTCAGCCCTG GCTGGTATCC AGGCTCTTGA CACAATIGCA AGAAAGAGT
A1251 CAACCATCAC TTCGAAACA GTGAAAGTAC AGAGAIIIAI IGCAAAGIGG
A1A01 AAAAGTACAC ACTCAAGAGA GGGGAGCATG GGTGAACICC AGCGAAIGIC
41451 ATGTAAGGGG GGGTTTGAGG CTGCTGCCAT AATGGGTTTC TTTAACCAAG
41501 GGGTGAAACA TTCATGATGA TTCCTGAAAA AAGATGGAGA TTTCTTGGAA
41551 CTGTGGTGCC AGCTATTTTT ACACCAAATA TGAATGTTCC TGGAACTGTC
41601 ATGGTGCTGG TGGGTGTATG ATTTAGTATG TTAATGAGTG TATGATGAGG
41651 TCCTAGGTGA AACCTAGGTC AAATCCAGCA CAATGGAGAG GACCCACAGA
41701 CTCTCTGAAG GAAACGACTG CTCCTGCAGG ACCCAGGCAA CTCCCCCAAA
41701 CTCTCTGAAG GAAACGACTG CTCCTGCAGG ACCCAGGACC CTCCTCTCCC 41751 ACTGTGAGTA CCCCAACTGT GGAGGTGGGA AAGAGAGACC CTCCTCTCCC
41/51 ACIGIGAGIA CCCCACTGI GGAGGTGAAC CTCTCTTGC TGGAGAAGTT
41801 AAACACACA CCCCACTGGA GAAGCTGAAG GTCTGTTTGC TGGAGAAGTT
41851 TCTGACTITA CCTGGAGCTG AGTGGACTTG AAGAGCCCAG TGAAATACAC
41901 GGGGAGAAGA AGCAGCAGAA AGGCCCTGGG AGCTTGCTGG GTCCACAAGC
41951 AGGCCATTCC TGCCTGCAC CACAGGGATC CAATGGGAGA GGAGCGGGGG
42001 TAAAATTCCA TAGGGAGAAG CAAATCTCTA GCTGAACTTG GTGACAATTT
42051 GAACAGGGTG AGAAAGCGCC TGGCCAGAAC TCAGGAGAGG GCACAAATCC
42101 AGTGTGCAGA CTCCGGGGGC AGGGGATAAA CCAAGCTCTT TTATTTCCCA
A2151 CCTCCCACCC CCGACCCTGG GGCAGGTTTT CAAGCAGGIA IIGCIICICI
ADDOL ACTTAGAAAC AACCTGGGAG CTGTGTTGGC GGGGGAGGGG GGIIGGGAI
A2251 CCCCCACGC CGTGGTGGAA AGCACGGTGG GAGTGAGACC GGCCCTTCGG
ADDA TITTOATOGO AGOTGGGTGA GGCCTGTGAC IGCCAGCIII ICCCCACIIC
ADDED CTCACAATCT CCATGTTTCT GCAGAGACAG CCATAAICCI CCIAGGIACA
AZANI CAACTCCAGT GACCTGGGAA TCCCACCCC ATICCCCACA GCAGCAGCAG
AZASI CAGCAAGGCC CACCCAAAGG AGTCTGAGCI CAGAGACACC TAGCCCTGCC
ADENI CCCACCTGAT GGTCCTTCCT ACTCACTCTG GTATCGGAAA ACAAAGGGCA
ADEEL TATAATCTTC CCACTTCTAG GGCCCTGCCC ACTGCCAGII ICICCCCAIA
ADENI ATACCAAACC TCATCCTCTC TGGAAAAGCA CLACCICLIG GCAGGAGGAC
12651 AACAGCACAA AAATAGAATA TTAACCAAAG CTAAGAACCC TTACAGAGIC
42701 CATTGTACTC CCTGCCACCT CCACCAGAAT AGGCACTGGT ATCCACAGCT
42751 GAGAGACTCA TAGATGGTTC ACATCACAGG ACTCTGTGCA GACGACTTCC
42751 GAGAGACTCA TAGATGGTTC ACCTAGCT GGGTGGCTAG ACCCAGAATA
42801 AGTACCAGCC TOGAGCTOGG TAGGCTCACA AGAAACCATA TCCATAGGAA 42851 GAGATAACAA TCACTGCAGT TCAGCTCACA AGAAACCATA TCCATAGGAA
42901 AGGAGGAGAG TACTACATCA AAGGAACACC CAGTGGGACG AAAGAGTCTG
42901 AGGAGGAGAG TACTACATCA AAGGAACACC CAGTGGGACA AAAGACTAGTA 42951 AACAAGACTT TCCCTCTGAA AGAGCCTACC CAAGTGAGAA GGAACCAGTA
42931 AACAAGACII ICCCICIGAA AGAGCCIACC CAAAAATCAC ACTAGTTCAC
43001 ATATGACAAA ACAAGGCTCT TGATGCCCCC CAAAAATCAC ACTAGTTCAC
43051 CAGCAATGGA TCCAAACCAA GAAGAAATCC CTGATTTACC TGAAAAAGAA
43101 TTCAGGAGGT TAGCTATTAA GCTAATCAGG GAGGAACCAG AGAAAGGTGA
43151 AGCTCAGTGC AAGGGAATCC AAAATATGAT ACAAGAAGTG AAGGGAGAAA
Α2201 ΤΛΤΤΟΛΛΟΌΑ ΛΑΤΛΟΑΤΑΘΌ ΤΤΑΑΑΘΑΑΑΑ ΑΑΚΑΑΙΑΚΑΑ ΑΑΙΙΚΑΘΘΑΑ
12251 ACTITAGACA CACTITAAAA ATTGCAAAAT GCTCTAGAAA GTGTCAGCAA
ADDOL TACAATTCAA CAACTAGAAG AAAGAAATTC AGAGCICGAA GACAAAGICI
43351 TCAAATTAAC CCAATCAAAC AAAGACAAAG CAAAAAGAAT AAGAAAATAT

43401 AAACAAAACT CCCAAGAAGT CTGATATTAT GTTAAATGAC CAAACCTAAG
ARASI AATAATGGGT GTCCCTGAGG AAGAAGAAA TTTTAAAAGC IIGGAAAACA
ASSOL TATCTGAGGG AATAATTGAG GAAAACTTCC CCGGCCIIGC IAGAAAICIA
ΑΣΕΙ ΟΛΟΛΤΟΟΛΛΑ ΤΑΘΑΔΕΔΑΘΌ ΑΓΑΔΑΔΑΔΑΘΑ CCTGGGIAAI ICAICGCAAA
AZENI AAGGTATTTG CTTAGGCACA CTGTCATCAG ATTAICCAAA GITAAGATGA
A3651 AGGAAGAAT CTTAAGAGAT ATGAGACAGA AGCACCAGGA AACCIACAAA
ARTOL COMMACCEM TEMPATEMENT AGCAGATTE TEMPAGAAA CCCIACAAGC
ARTEL TAGAAGGGAT TGGAGCCCTA TCTCTGGCCT CCTCAAAACA ALIALIAGUU
ARROL AAGAATTITG TATCCAGTGA AACTAAGCAT CATALAIGAA GGAAAGALAC
A3851 ACTCATTTTC AGACAACAA ATGCTGAGAG AAATTGCCAI IACCAAGICA
ARONI CCACTACAAG AACCGCTAAA AGGAGCTCTA AATCITAAAA CAAATCUTGG
ARGET AAACACATCA AAATGGAACC TCTTTAAAGC ATAAATCACA GAGGATCTAC
ΑΛΟΟΊ ΑΛΛΑΤΛΑΔΑΚ ΤΑΓΔΑΘΤΤΔΑ ΑΚΑΘΓΑΚΑΚΑ ΓΑΚΑΚΙΓΙΚΑΚΑ ΑΚΑΚΙΓΙΚΑΚΑ
MANSE GENERAGE GACCACCCC ANNAMATET GAGTGCTCCA ACTUIGGAAG
AA101 TAGGAAAGGA AGAGCATCCT TTCCTGAACA CACACCCCCA CIGGAGAAGC
AA151 TCAACGTCTG TTTGTGGGAA GAACAGCTTT AGCTCTTTII IGGIIIIIIG
AA201 GAAAAAACC CAAAGTACAC AGGCAACAAA GAGCAIGAIG AAIGCCAACG
11251 CTACCCTCAC ATTTCAATAC TAACATTGGA AIGIAAAIGG CCIAAAIGCI
44301 CCACTTAAAA GATACAGAAT CACAGAATGG ATAAGAACTC ACCAACCTAC
44351 TATGTGCTGC CTTCAGGAGA CTCACCTAGT ACATAAGTAC TCACATAAAC
44401 ATAAAGTAAA GGTGTGGGGA AAGGAATTTC ATGCAAATGG ACACCAAAAG
44451 CGAGGAGGG TAGCTATTCT TATATCAGAC AAAACAAACT TTAAAGTAAC
MASOT ACCACTTADA AGAGAGACAA AGAGGGACAT TATATAATUU TAAAAUUCCT
44551 TGTTCAACAG GAAAATGTCA CAATCCTAAA CATATAAGCA CCTAACACTG
44601 GAGCTCCCAA ATTTATAAAA CAATTACTAA TTGACCTAAG AAATGAGACA
44651 GACAGCAACA CAATAATAGT GAAGGATTTT AATACTCCAC TGACAGCACT
44701 AGACAGGTCA TCAAGAGAGA AAGTCAACAA AGAAACAATG GATTTAAACT
44751 ATACCTTGAA ACAAATGGAT TTAACAGATA TATACAGAAC ATTTCATCCA
44801 ACAACTGCAG AATACACATT CTATTCAACA GAGCATGGAA GTTTCTCCAA
44851 GATAGACCAT ATGATAGGCC ATATAATGAG CCTCAATAAA TTTAAGAATA
44901 TTCATATTAT ATCAACATTC TCTCAGACCA CAGTGGAATA AAACTGGAAA
44951 TGAACTCCAA AAGGAAACTT CAAAACCATG CAAATACATG GAAATTAAAT
45001 AACCTGCTCC TGAATGGCAT TGGGTCAAAA ACAAAATCAA GATGAAAATT
45051 TAAAAATTCT TCAAACTGAA TGACAATAAT GACACAACCT ATCAAAACCT
45101 CTAGGATACA GCAAAGGCGG TGCTAAAAGC AAAGTTGATA GCCCTAAACG
45151 CCCACATTGA AAAGACTGAA AGAGCACAAA CTGACACTCT AAGGTCACAC 45201 CTGAAGGGAC TAGAGAAACA AGAATAAACC AAACCCAAAC CCGGCAGAAG
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45401 ATCTAGATA CCTCAGAGA AATTGAACCA CTATGAACAC CTTTATGCAC
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45551 TCTCCTAGCT TAAATCAGGA AGAATTAAAT ACCCTGAACA GATCAATAGC
45501 AAGCAGCGAG ATTGAAACGG TAATTTAAAA ATTACCAAGA AAAATGCCCA
ASSS CONCORDE CATTOACAGO AGAATTATAT CAGACALICA AAGAAGAALI
ASTOL COTACCAATT CTTTTGACAC TAAGGAAACC TCCCCIAALL CALCCIALGA
45751 ACCCAGCATC ACCCTAATAC CAAAACCATG AAAGAACATA ACCTAAAAAG
ASON ANACTOCAG ACCAATATCA TTGATGAACA CAGATGCTGA AAICCIIAAC
ASRS1 AAAATACTAG CTAACTGAAT CCAACAGCAT ATCAAAAAGA IAAICCACCA
45001 TCATCAAGTG GGTTTCATAT CAGGGATGCA GGAAIGGCII AACAIACACA
45051 ACTCAATAAA TGTGACACAC CACATAAACA GAATTIIIIA AAAAATCACA
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AGOST TITATGATTA AAACCCTCAG CAAAATCAGC ATACAAGGGA CATAGGCCTT
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46151 CACATTCCCT CTGAGAACCA GAATGAGACA AGTATGCCCA CICICACIGC
46201 TCCTCTCAA TGTAGTACTG GAAGTCCTAG CCAGAGCAAI AAGACAAGAG
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16351 CAAACCTCCT AGAACTGATA AAAGAATTCA GCAAAGIIIC CGGAIACAAG
AGADI ATTAATETAE ACAAATEAGT AGETETEETA TACACCAACA GCAACCAAGI
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46501 CAAAACA	AAA CAAGACAAAA	CAAAAAAACA	AAAAAAAACA	AATACTTAGG
46551 AATATAC	TTA ACCAAGGAGT	AGAAAGACCT	CTACAAGGGA	AAATTACAAA
46601 ACACTGO	TGG AAGGAATCAT	AGATGACACA	AACAAATGGA	AACATGTCCC
46651 ATGCTCA	ATGG ATGAGTAAAA	TCAGTATTGT	GAAAAATAAC	CATACTGCCA
46701 444664	ATCT ATAAATTCAA	TGCAATTTCC	ΔΤCΔΔΔΑΤΑC	CACCATCATT
40701 AAAGCAA	AGAA TTAGAAAAAA	CAATTCTAAA	ATTCATATGG	ΔΛΟΓΔΔΔΔΔΔ
46/51 CITCACA	AGAA IIAGAAAAA	CAATICIAAA	ALLCATATOG	ATCTCCACCC
46801 GAACCTC	CAT AGCCAAAGCA	AGACTAAGCA	AAAAGATCAA	TCACCAAAAC
46851 ATCACAC	TAC CTGATTTCAA	ACTATACCAT	AAGCCCACAG	ICACCAAAAC
46901 AGCATGO	STAC TGGTACAAAA	ATAGGCACAT	AGACCAATGG	AACAGAATAG
46951 AGAACAC	CAGA AATAAACTCA	AATACTTACA	GCCAACTGAT	CTTTGATAAA
47001 GCAAATO	GAAA ACATAAAGTG	GGAAAAGGAC	ACCCTTTTCA	ACAAATGGTG
47051 CTGGGAT	TAAT TGAATAGCCA	CAAGTAGGAG	AATGAAACTG	GATCGTCATC
47101 TCTCAC	CTTA TACAAAAATC	AACTGAAGAT	GGATTAAGGA	CTTAAACCTA
47101 TCTCACC	GAAA CTATAAAAAT	TOTACAACAT	AACATTGGAA	AAACCCTTCT
4/151 AGACCIO	JAAA CIAIAAAAAI	CTTTCATCAC	CAACAACCCA	AAACCAAATG
4/201 AGACAT	TGGC TTAAGCAAGG	GITTCATGAC	CAAGAACCCA	AAAGCAAATG
47251 CAATAA	AAAC AAAGATAAAT	TGCTGGTACC	IAATTAAACT	AAAGAGCIII
47301 TGCATGO	GCAA ACGGAAGTCA	GCAAACAGCC	CACAGAGTGG	AAGAAAATCI
47351 TCACAA	TCTA TACATCTGAC	: AAAGGATGAA	TATCCAGAAT	CCTACAATGA
47401 ACTCAA	GTAA ATCAGTAAGG	: AAAAAACAAT	CCTATCAAAA	AGTGGGCTAA
47451 GGACATO	GAAT AGACAGTTCT	CAAAAGAAGA	TATACAAATG	GCCAGCAAAC
47501 ATATCA	AAAA ATGCTCAACA	TCACTAATGA	TCAGGGAAAT	GCAAATCAAA
47551 ACCATA	ATGT GATTCCACCT	TACTCCTGCA	AGAATGGTTA	ΤΔΑΤΔΔΔΔΔ
47551 ACCATA	AAAA AACAGCAGAT	CTTCCCATCC	ATCCACTGAA	CAGGGAACAC
4/6UL AAAATC	AAAA AACAGCAGA I	GIIGGCAIGG	CTACACCCAC	TATTCAAAAC
47651 TITCTA	CACT GCTGGTGGGA	AIGIAAACIA	GIACAGCCAC	TATIGAAAAC
47701 AGTGTG	GAAA TTACTTAAAG	AACTAAAAGT	AGAACTACCA	TTIGATCCAG
47751 CAATCC	CTCT ACTGGGTATO	<b>TACTCAGAGG</b>	AAAATAAGTC	ATTATICAAA
47801 AAAGAT	ACTT ACACATGCAT	T GTTTACAGAG	CACAGAGTTG	CAACCCAAAT
47851 GCCCAT	CAAT CAATGAGTGO	<b>ATAAAGAAAC</b>	TGTGGTATAT	GTATACATGA
47901 TGGAAT	ACTA TGCAGCCATA	AAAAGGAATG	AACTAACAGC	ATTTGCAGTG
47051 ACCTCC	ATGA GATTGGAGAG	ΤΔΤΤΔΤΤΟΤΔ	AGTGACGTAA	TTCAGGAATT
47931 ACCIGG	CAAA CATCATATGT	TCTCACTGAT	ATGTGGAAGC	TAAGCTATGA
40001 GAAAAC	CAAA CATCATATG	CATACAATCO	ACTITICAGA	CTTAGGGGGA
48051 GGAIGC	AAAG CAATGAGAAT	GATACAATGG	TACALATOTO	CTCTACTCTA
48101 AGAGTG	GGAG GGGGGCGAGG	GATACAAGAC	. TACAAATGIG	GIGIAGIGIA
48151 TACTGC	TCAG GTGATGGGT	G CAACAAAATC	. TCACAATCAC	CACTAAAGAA
48201 CTTACC	CATG TAACCAAAA	CACCTTTACC	: CCAATAACTT	ATGGAAAAAI
48251 AATCCA	GCAC CACATTAGG	T TTAGTCGGAC	TTAGCCAGCT	TGGCTTACAC
48301 CCTGGT	TITT CAGGITCITA	A TCATTCCCAG	TTTATGCAGC	TGTTTCAACA
48351 TTTTCC	TTTT GCTAGTCAT	G TGAAACTGCT	GTCTGGAATT	TTCTTTTCTC
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48601 TTGTCA	CAGT TCCCCTTGT	COLLEGE	AIAIAIAIAI	CTTACTACTT
48651 ATTGTA	ATTA AATATGCTG	A CTGGGAAGGA	GIICAGAIGI	CITACIAGII
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49551 ACCCT	IAGCA AICAICAAA	i idectifict	, cccicicio	. IGCAICCIGA

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SOSSI CONTACTOCO TTOTOCTTTG GGGAGGACIC AGGAAGCIIC CAAICAIIGI
COANT CCAACCCAAA AAGGGGAGCA GGGCATCTCA CATGGTGGAGCA GCAGGAGCAA
ENALL CACACACCAC CACACACTCA CTACACACTT TTAAAIGACC AGCICICIA
SOSO1 AGACCTCTAT CACGAGAACA GCACCAAGAG GAIGGIGA AACCAIICAI
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SOGST ACCATATOAG TGAGTAATTT ACTTCATCAT TITLAAGICA CAIGGLIATA
- COZOL ACATAGGGTT AATGTGTGTA ACTTIACAII IAIAAAIGAA AIGAAIAAAG
ENTEL TOOTATOOCO AGTACCCAGO ACATAGTAAC AGGIGICIIA CAAAIAIICG
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EDDO COCCOCACTOT TTCCCAGCAT AGTTGATTCC CCAGGIGGCI IIIGIIAAII
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EDANI CTCATCTT TGTCCCTGTG GATAGAAGGG GICCACAIGI GGIIICAGGA
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EDENT TOCACCOCAG ACCTTGAGGA TGCCCACCTG GGAGCACAGA IICACIIIGC
52651 CCAGAATGTA CACTCCAATT AGCAGCAGTT ATAAGTGGGG TTTTAAGAAA
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52701 AAAAGACAAG GCAGTTCCTA AGTTATTTAC CAAAAATTTA CATTAAAATA
ENTEL ATOTALOCTA TIGATOGACT ALGUALIALI CILIMINICA CARRITACA
- FOOR 1 - A A TA CTCTC CTTC ACCATC (G)
52851 AAATACTGTC CTTGAGCATA GATTTGTGCA TATCTCATAT AGCTCAGACT 52901 CATGTTTCTC TAAACCTAAT AAATTGTGCA TATCTCATAT AGCTCAGACT
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52901 CATGITICTE TARGETIATION TO TOTAL TOT
FORTH TOACCAACTE ACTECTECAT IGGIAAAG IGGIAATICCE AGAIGGICEI
COLOR CTCCCACATT TCCCCCCAAGG GGAAAGGAIG AGICIIAGIG GGGAIIII
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FOADI AACTCAACTA AAAACATCAI GAAGAAAAII AAAAICCAGI CCIIICIING
FOART ACACTTCTTC TACCACCAAA TAATILAAGA TITAGATOO ATTOTAGGAA
FORES PROFESTANTE TECTECTORS CONTABILIS SCIENCIAL SILVACIAL
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ESSES CONTRACTOR ATTACACTTT INDADGGG IC IC ICIAAACIAG AIDIIGASS
PROOF CAATAATTCA CCATCAAACT GCCIGIAGLA ILIALAIAAA IIQQUIQAAI
FORT TTCTCCCTTC TTCACGTT() GADALALALI GAGGILICIA GGCCIGION
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FERNA ATTECETTAT CECTETACIA LALABOAROL IGACALAMCA ALCOLONIO
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FESES ATATOTOXXX XCTTXTTTCG AGGIAAAAAA AAAAAAAAAAAAAAAAAAAAAAAAAA
FERMI CTANATITTA ATTTCANATA TGATILIGGA AAGILIGICA AAIAICAAA
- FEDES CTTAAAAAA CTTACTCAAA AAAA CTTACTCAAA AAAA AAAA CTTACTCAAA AAAAA AAAA CTTACTCAAAAAAA AAAA CTTACTCAAAA AAAAA CTTACTCAAAA AAAAA CTTACTCAAAA AAAAA CTTACTCAAAAAAAA
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FEED1 CCACACCATC ACCCAAACTC TICCLULI HIIAIAAUUA AIGICAGAII
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FECOS ************************************
55601 TITITICIG TITITICITITI TGAAGAT TCTTATTCAA AGGAGAATGC
55651 TTACTGTCTC TTATTAATAC TATATAAAAT TCTTATTCAA AGGAGAATGC
- FERM CAAAFTTATA TTACTCTCTCT GILAALALA AAGULAALI I IMMIINOON 🗠
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55801	ATTTTCATAA	ATCTTTTATA	ACCTATTACA	ATTTTCTATT	AAAGAGAAGA
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56051	TTTTCTCCTA	TACTTCTTTT	ATTTTGAGAC	GGAGTCTCAC	TCTGCCCAGC
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2010T	CIGGAGIGCA	GIGGCAIGAI	CICGGCICGC	ACTACCTCAA	ACTACACCCA
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56301	TTAGGACAAA	ATCTACTTTC	сттстссст	TATCATTTIG	ACCACACAAT
56351	GCTCTCTTTC	ATGCAAATGA	AAAATTACTG	TCATTTCAAC	TCCCTTTACC
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56851	GGAAGTAATT	TTGAGCTGTT	TTATGCCAGT	ATTTATAGAT	GAAAACCATT
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2/00T	ACACAATGCT	CAAAACTTCA	TTTATACACT	TCTATCTCAT	TTACATTCAT
2/U2T	TITIGAAACT	GAAAAGIICA	TTAACAATTA	TCTATCTCAT	CTTCATTAAA
2/10T	TIAATTIAGI	TIATICATIC	TTATECTTA	TGCTTGAATA	TTTATACCCT
2/12T	CAAAAGTAGC	CACCATCAAG	HATHCHH	GTTAATCATT	CCTAAAACAC
5/201	GCAAATGTCA	GGCAGTTGCC	ACCTAAGCAA	GAACCCGAAA	GCTAAAACAG
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				CTGGAAGGGA	
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59201	AAATAGGACT	GCTTTCCTGA	CTGGGAATCA	AACCTGGGCT	GCAGTCATGA
		TTAGCTGGTA			TTTTGTAAAT
59301				CATATAAAGG	
			•		
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59401		AAAGATATGA			GATTGTGAAG
59451	TCCAGCAGGG	CATTTGAAGG	ATATTGTCTG	GGCCGGGCAT	GGTGACTTAA
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		AGGAGTTTGA			TGAAATCCCA
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59701		TGTAGTGAGC			CTATCCTGGT
59751	GACAGAGCAA	<b>GACTCTGTCT</b>	CAAAAAAAA	AAAAAAATA	CTATCTGATG
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59851		TCTGTATTTT			TCTTGTTCTG
59901				AATTATCTTC	
		-			
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	GAAGTAAGTC			AAACTAGCTT	TTTCTAATTG
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				GATCTCACGC	
					AAGAAAGTAA
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				CCCGTATCTT	
				AACTGTCTGG	
				CCTATTTAAG	
61301	TCTGGTTCAC	ACGCCTCTGA	CAGTACCAAC	ATTCCAATTG	TCACGAACTT
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				GCATAGATTC	
				TGGGTTTCTA	
				ATTTACGTTA	
61601	AGCTATTGAT	AGGCTACACG	TTATTCTTTG	TATCACAAAT	TCCAGGATCA
61651	CGATGATAAT	GAGCCAGGCA	<b>GCTAGTCAGA</b>	AACAAAATCC	CAGGCATCAG
				TGTCTCTCTG	
61751	ATTITECATA	GTTCATATAG	CTCAGCCTTC	TCTGAGCTAT	TTCTCTCTTC
61001	TCACTCCCTT	TCCTCCAACC	ACCCTCCATC	ATATGTGACT	CACACTCCTA
				AACTCAAGGT	
				TTAGTAGTGT	
61951	TGGGTTTTAC	ATATATTATC	TCATTTATTC	ATCATAACAA	CCTGGTTGAT

TATTECTEAN CANACTENES CTCANAGGAG
62001 AGGGATTATT ATTCCCATTC TATTCCTGAA GAAACTGAGG CTCAAAGGAG
CODE CTARRATT TTCCTATAGT (ACACAGCIA GGAAGIGGCA GAGCGAGGAC
COINT TOWARCOOK CANTOCTGAC III AAAGCLI CIGCICIICC IGCIGCACIA
COLET TACCATCCCT ATACACATCT CTGAGACICE IGIAAAAAIA IGIAAGGAAC
COOM ACCAPTEATE TOATTTATTE TOTALE ALAL CCLACAGGA TACAACCIO
CODE 1 CTARCCCACC TATCTCTGTA TGTTTTTAL CALIGULICA TICCCCATCT
62301 TCCACAACAG TGCCTACCGC ACAGTAAGTG CTCGATAAAT ATCTTTTAAA
62301 TCCACAACAG TGCCTACCGC ACAGTAGTTT AGGGCTAAGG CCTTTGGCTT 62351 TGAGCATGTG AATGAATGTG TGTTAGTGTT AGGGCTAAGG CCTTTGGCTT
62351 TGAGCATGIG AATGAGTIA GCACACTCAC
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COART AAACATACCC TCATATAATC ALAIGCACII CAGIIICIII GCAGGICCIO
COEDI COTTOACACA AATOTGAGTT TGAATTTCTG LICCACCACI GUGIAACIUA
CARRA CTCAATTTCC TCACTTAIGI IIGGIAIIII ACIIAGIIIC CICACCIVIA
COCOL ATTACCANTA ACAGGAATAC TCATGTCAGI ACIACIIIGA AIGACAGIGA
COCET TAACAATATC TACTTCAAGC ACCICALAAA GIACGIGGII GAIAAA GA
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COOM CTCTCACAAA CAATAGATGA TAGICIGIGG IIGGGAGAIC IGAICAIGGG
CODE 1 CACCTCCTCA CAGAATGCCT GGTTGTTTAL TICACTAATG TATTTTTT
COLOR TOOTATACAT ACAAATCATC TCCATGAAAG GIAGCIIIIC AGGGIACIC
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COART CACAAATATC TCCTCTATTA GTTTTCCGTT GCTGCGGTAA CAAATTGCCA
COEDI CANACCTECT CECTTENENE ATCATAGNII INGINICIIN CANIICION
COEET ACTORORACT CONNATORS TOTOO TAGG CIAAAAICAA IGIGICACCA
COCAL COCOTOTOTT TOTTOCAGAG COTOCAGGIG AGAAICIGII ICAIIAICII
COCEL TECTACCTEC TECACCCTCC CTGTATICIC GGCIIGIGG CCCIICCIII
63701 ATCTTCAAAG CCAGCAGCAT ACTATCTTCA AACCTCTCTC TGACTCTGAC
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63851 TCCCTTTTGC CACAAAGAA AACATATTTG CAGGTTCTGG AGATTATAAT
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CANNO CACTTTTAC TATCTATGO ALLI ALAAGA LIGULIALLI CAAGAAA
CAREL TITATTOTAN TICTITITITG TIATCANCAL ANAGLANICA ANAGGOTONO
CA101 AATCTACTET AAACTCACTT TATTCGAGIA CAAAGIIIGA GGACAAGCCC
CATEL CCCACCAAAC AGAATTCAAG GAATGGAAGI CAGAGIICCA AAGIGIAGAC
CAREL CATCETTCEA TOTARGOTTE ANIGONIAGO INCARCACIÓN INVITAGICA
CARRI AACTCCTCTT TIICIIIIIGA GAAAIGIAIA IIIAAACAII CIAGIGIGIGI
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64501 GAGGTAAGCT ATAATCTAAG ATGCACCCCTT GTCAAAATCA ATTTAGAAGA 64551 ACTCAGTTTC CAGGGCTTAA CTTCCCCCTT GTCAAAATCA ATTTAGAAGA
- C4CA1 TCCTC444TT TTATTTATI LIAIALIIAL ALIALIMMMU MIQLIIICII
CACEL ACAATCTTTC ATTCTTCTGG GGAGAALICC LAAALICCL AAGCALAAAC
CAZOL ACTOTTOTT TOTTTOAGL ALALALILUL LUUCAGLACA IGIIAIIII I
CATEL ACCTAACTCT TCTCCCATCC CAATAGAGAL GCAALGGAGG ICAAALICCA
CARRI TOCTITITAG AGGAATCTAT ACAAATTAGA GCIAGIAAGG AIAIAAAAGA
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CARRIE TAATCTAAAA TCCTGTTAAA AGAAGACGCI ICCCAAIAII CAAGGGCIGI
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65UUL ATGIAACAAA CIGCCCCAAA ACIIAITAAC TOAAACAG ATGIATTAAC
65051 GTCTCATGAT TCTGTAGATT GGCCAGGAAG TTCTTCCAGT CTGGGCTGTT

65101 ATGTGAGTCA GTGATTCAAA ACTATCCATC TAGGCCTTGA AGGCGGGGGC
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66501 AGGGGAGTCT GCCATCCTGG AATCTTCCACAGGTCA AGAAGAAGAA 66551 GGAAGGAGGG AAAACCATTT CAGATGCTGC TGCAAGGTCA AGAAGAAGAA 66551 GGAAGGAGGG AAAACCATTT CAGATGCTGACAA GATAAATATT GTGACCTTGT
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- 44664 AAAAFAFAFF CACATTCITC (ACAALIIII III III III AUUIU AUUIU
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67/51 TAGTATACTT TAGCTGAGTA GAGTAGCTGAG AGCACCTCTC 67801 TGTCGTGCTC GTGTAGTAAC CTGTTCTAGT CTTGCGTGAG AGCACCTCTC
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67901 ACAGTAGGAC GTCCGCACCA GAGTTTAGTT CGGGTGGAGA GAGTAGCCTT 67951 TGTACTAGTA GTGTAGTATA GTAGTACACG GAGTAGAG GAGTAGCCTT
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68101 TCTACACATA TTTTGGAATA TAAACTTAAG 68151 GGGTTTACAT AGGTTTAGCT GGCAAACAAT TTTCCAAAGA GCTTGTGCCA
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68201	GTTTATACTC	ACATCCGCAA	TGTATGAAAA	GTCAAGTTGC	TCCAAAGCAT
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68301	TGTGTAATGG	TATCTCCCTG	TGGTTTTAAT	TTGCATTTT	CTGGTGACTT
68351	ATGAGTTTGG	GCATATTTTT	GCTTATTGAC		CCCTTTGTTG
68401	GGAAGTGCTT	GTTTGACTCT	TTTAACCATC	TTTCTATCGG	TTGCCTCTTT
68451	TTCTTATTGA	TCCATGAAAG	CTCTTTATAT	ATTCTATATA	CAAGTCTTTT
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	TOCACCTCCT	CAAATCCACC	ACAACCAAAT	TTTCAGAAGA	TATETEECAA
68551	TCCAGGTGCT	GAAATGGAGG	AGAAGGAAAT	TOTTATTTOT	TACTATCAAC
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68701	TTATATATAA	TATTTTATAT	TGTATCATAT	ATAAAATCAA	CAGATTTTAA
68751	TTAATTCAAA	ATTCAGTATC	TTCACTGACA	TGTGTTAGCT	TCCTAGCACT
68801	<b>GGAATGTCAT</b>	TTGCTTGCTT	ACATATAAAG	GTATAATAAA	ATTTTAAATC
68851	TTCTGCTCAG	ATAAAGAAGT	<b>AGTGAATTAT</b>	CTAAGATGTT	TGGAATGACT
68901	TAACATAAAT	ATTTCTAAAG	<b>GGAAAGGGAT</b>	AAATCACATA	ATTTTTCTGC
68951	ΑΤΓΙΙΑ	ΔΑΤΔΔΔΔCΔΔ	ATAAAAAGAA	AGATGCGTTT	ATCAGTAGGG
				GCCTGACAAT	
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69301	GTGAAACTTC	ACCAAGAAGT	CTTTCTTTGG	GGCATATAAA	CIATITICAC
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69451	CGTAGTGATT	TCTGTGTTCT	CTTTAAGAAA	TTTTTGTCTG	GCTGGGGACA
69501	GTGACTCACG	CTTGTAATCC	CAGCACTGTG	GAAGGCCGAG	GCAGGCAGAT
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69701	AGGTGGAGGT	TGCAGTGTGC	CGAGATCATG	GCGCCAATGC	ACTCCAGGTT
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70001	ACCATCTATG	TATEGETTTE	CTGACTCTGT	TCCATTGATT	CATTTGTATA
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70101	TTTCACTAAT	TCATCTTTCC	ATTATETTEE	CTACAGTTGG	ΤΤΟΤΤΤΔΔΔΔ
	TTCCATATAA	ATTTCATAAC	TACCTTTTCA	ATTTGTATTT	TAAAGCTGCT
70151	CCTATCTATA	TTCCCTACAT	CCACTCTATA	GATTAATTCA	CCCATAACTA
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	ACATCITII	AAAATATCAA	ATTACATAT	ATATCCCTAT	ACATTTCCTT
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/0401	. AGAGGICIAG	CGIAITIGIC	IIIAGACIGA	TGACTAGGTA	CTTTCCTCCT
/0451	. TTACAAGTGG	TALIALITAL	CAAAATIGTA	TTTCTTGCTA	GITIGGIGCI
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70651	. тсттсссттт	CAATCTTGCC	тттсттсс	ATGCATATTG	CACATGCATT
70701	. GAGAACAATG	TTGAATAAAA	GTAGTGATAA	TGGACATCTT	TGTCTCTTTT
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71151	CTACATATAT	TTTAGGATGT	ΑΓΑΤΑΘΑΓΑΑ	GTTTGAATGG	TAACAAGAAT
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71751	TGCCAAGTCA	GGTCCTCCAC	GTGGTGAGAT	GAATGTGACT	CAGGGCACAG
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71301 GTGAATGAGC TGACCTTAGG TGGAAGTGGG GACCCTTCCT TCATGTACTA
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THUSE WATTAILETA CETCAGETE CAMADIAGET GOSTIMULES MEGATIONS

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74EO1 TOCCOCTTOC ANNOTOCTOG GATTACAGGI GIGAACCACI GCCCCGGCC
TATEL TO A CACTTA CTATA A TATA TATA LIGILAGI LICILI CACA LICALICIO
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TEDAL CACCCTTCCA ACTCCACCCT GCGGGAALL ATGAATATOC CACAGCACTC
- 78381 CACCCCCCC TACACACACA (486   166   166   1888AAAAAAAAA AASAAAAAAAA
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TEACH TITATATATAC CCAAAAACCG GGAAACAACC IGAALALICA ICAAGIGGGG
TERM ACACCTTCAC TAATCATGTG ACATACALAA ALIGUAGGAC IGCACACIIG
TEEL ACAAAACAAC TCACAAATGT (1(   Allill   1 Adididdil idcicicca
TECAL ACTATACTCT TAACTCAAAA AAGCACTGTG GCCTCAAATI TATCTATAGA
TEGET TTCTATACAA TCCCCATCAA AAICICAGCI GGCIICIIIG CAGAAAIICA
TOTAL CARCETCATE TTARRESTE LA LAGABATE CARGUNACIO MARRII CARI
TETEL ANATTONNO NOTROCCANA ACANTOTICA ARARGARGAG CARAGIIGA
TERM COCOTONTAC TITTONGTIT (GAAAGIIGI IAIGAAGCIA CAAIAAICAA
TEGET CATACCCTCC TCCTCCCAIA AGGALAAALA IGGAALAGAA IIQAGCAISI
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TEGET ACAAAATTCA ATGGGGGAAG AAIIIGILII IILAACAACI GGIGGIGGA
76001 CAACTCTATA TCCAAATGTA AAAGAAIGAA AIIGGAACCC IACCICACAC
TOOLI CATCTACAAA ATTAGCTCAA AATGGAAAAC AGAGGIAAAI AIAAGAACII
76101 AATGTATAAA ATTCTTCGAA GAAAATACAG AAGTAGATGA TCAAGACCTT
76151 GTAATCACTA ATTGTTCCTC AGATATGACC CCAAAAGAAC AAGTACTAAA
76201 AAAAAAAGTA GACAAATTGG ACACCATCAA AATTGAAAAC TTTTATGCTT
76201 AAAAAAAGTA GACAAATTGG ACCAAAAAAGT GAAAAGTCAC CCCAGAGAAT 76251 TTTATACTTC AAAGTCACTA TCAAAAAAAGT GAAAAGTCAC CCCAGAGAAT
76301 GGGGAGAAAA TATTTGCAAA TCATATATCT ACTAAAGGAT GTGCATTTAC
76351 AATATACAAA GGGGCCAGGC GCTGTGGCTC ATGCCTGTAA TCCCAGCAAA
76351 AATATACAAA GGGGCCAGGC GCTCGCTGA GGTCAGGAGT TCAAGACCAG 76401 TCGGGAGGCC AAGGTGGGTG GATCACCTGA GGTCAGGAGT TCAAGACCAG
76401 TCGGGAGGCC AAGGTGGGTG GATCACCTGA CTAAAAATAT AAAAATTAGC 76451 CCTGATCAAC ATGGTGAAAC CCTGTCTCTA CTAAAAATAT AAAAATTAGC
76451 CCTGATCAAC ATGGTGAAAC CCTGTCTCTA CTTACTTGGG AGGCTGAGGC 76501 TGGGTGTGGT GTCAGGTACC TGTATCCCCA GCTACTTGGG AGGCTGAGGC
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76651 AAACAAAAA AAACAAAAAA AAACAAAAAA AAAAAAA
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76/01 TTCCAAGTCA ATAATAAAAA CAGAAAATGC AATTGCTCAG TGAGCACTTC 76751 ATCTGAGTAG TTTTACATTA AAAGATAAAT AAATGGTCAG TGAGCACTTC
76751 ATCTGAGTAG TITTACATTA AAAGATAAA AAATGCAAA TCAAAATCAC 76801 AAAAGATCCT GAGCATTACT AAACATTAGA GAAATGCAAA TCAAAATCAC
76801 AAAAGATCCI GAGCATTACT AAACATTAGA GAATTACTTT TTTTTTTTTT
76851 AATGAGAIGI CATITATTA CATATTATA GAGAGAGAGA GTGTGTGTGA
76831 AATGAGATGT CATTICCTCT ATCTTCCAGG CTGGAGTGCA GTGTGTGTGA
76901 TIGAGACAGA ATCTTGCTCT AGCCTCAACA TCCTGGGCTC AAGTCATCCT 76951 TCATGAAAAT GGCTCACTGC AGCCTCAACA TCCTGGGCTC AAGTCATCCT
77001 CCTGCCTCAG CCTCTTGAGT AGCTGGGACT GCAGGCATGT GCCACCGCAC
77001 CCTGCCTCAG CCTCTGAGT TTGTAGACAC AGTGTCTCAC TATGTTGCCC
77031 CAGACAGTT GAAACTCCTG GGTTGAAGCA ATCTTTCTGC CTCAGCCCCC 77101 AGGCTGGTCT GAAACTCCTG GGTTGAAGCA ATCTTTCTGC CTCAGCCCCC
771E1 CAAACTCCTC TAACTATAGG TGTGAGCCAC CACACIGGGC CAGIACIAII
77131 CAAAGTGCTG TAAGTATAGA CAAGTGTTGG AGAGGATGTA GAGAAACTGG
TITEL ACCOUNTER A CATTGATAGT GGGAATGIAA IGIGGIACAG CCACIGAAGA
TO THE TOTAL ANACACTTCC ACACTTCTTC AAAAAGIIAA ACAIAGAGII ICCAIIIGA
77251 CCAACAATTC CCTTACTCAA TATTTACTCA AAALAALIGA AAGCAGGGAC
77401 TCAAATACAT ACTTCCACAC CAGTGIII AL AGLAGLALIA IIVAIAAIAG
77401 TCAAATAGAT ACTTGCACAC CASTGTTCAT CAACAGATGA ATGGATAAAC

77551 TAAAATICTG ATATACCTA CAACATGGAT GAACCTTGAA ATCTTATAAT 77651 AAATGAAATA ATCCAGACAC AAAAGGACCA ATATTATATG ATTCCACTTA 77651 GATGGAATGA CTTAGAACAGA CAAATGCATAGA ATTTATATAT 77651 GATGGAATGA CTTAGAACAGA CAAATTCATA GAACAGAAAA ATAAAATAGA 777701 GGTTACCAGG AGTTGGGAGAG GAGGAATAG GAGTTATTAT TAAATGGGTA 77751 TAGAGTTTCT GTTAGCAATG ATGAAAATGT TCTAAAAATG GACAGTGAT 77851 ATGGTGTTAGA ACATTCTGA ACGTACATAG GACACTGAA TTGTACTATA 77851 ATGGTGTTAAA ATGATAAATT ATATGATATA TATTATATTAC CACATAGA 77891 AAAAATACAA GAAGTTTACCA GTGGGGAAAA GGAGGGGTTA CAGAAAGACAA 77991 AAAAATACAA GAAGTTACCA GTGGGGAAAA GGAGGGGTTA CAGAAGACAG 77991 GAAAAATAGA ACGACTTTTC TCAGTATACC TTGTTTTTC TATTTGACTTA 78001 TGAAAATATG ACGACTTTTC TCAGTATACC TTGTTTTTC TATTTGACTTA 78011 ATATATCCAG TTTGTGGCAT AACCACACAA AAAAGAACAAAT TAATCCATAGA 78101 ATATATCCAG TTTGTGGCAT AACCACACAA AAATGAACCAAT TAATCCAAGTA 78101 CAAGAAAGAA CAGACAAATAT TATTAAACTAG AAAACCAAAT TAATCTAAAGT 78201 CAAGAAAGAA CAGACAATATT TATTAAACTAG AAAACCAAAT TAATCTAAAGT 78201 CAAGAAAGAA CAGCAAAAAT ATCTTAAAGT 78201 CAAGAAAGAA CAGCAAAAAT TAATAACAACAAA AATGAAACAAAT ATCCTAAATA 78201 CAAGAAAGAA CAGCAAAAAT TAATAACAACAAA AATGAACTA TTCCAAGTGA 78301 GGATAGAACC AACAAGATTT TATAATGAAA ATCTTGAGAATA TACCAACAGA 78401 AAAACTGAAAG CAACAAGATTT TATAATGAAA ATCTTGAGAATA TACCAACAGA 78411 TTTGAAATATG GTTAATTTTA AAATGTGTGA ATCTGGAATA TATTACAGATA 78501 TGTCACCCAG AATGTCTGAA ACAGGAAATA TACCAACAAATA 78501 TGTCACCCAG ATTGTCTGAA ACAGGAAATA TACAACAACAATA 78501 TGTCACCCAG ATTGTCTGAA ACAGGAAATA TACAACAAGATA 78501 TGTCACCCAG ATTGTCTGAA ACAGGAAATA TACAACAATAA 78501 TGTCACCCAG ATTGTCTGAA ACAGGAAATA TACAACAATAA 78651 ACATTATAAA TATTITTTAAA TATTITTTAAA TATTITTTAAA TATTITTTAAA TATTITTTAAA TATTITTTAAA TATTITTTAAA TATTITTTAAA TATTITTTAAA AATTGGTTAATTTT TACAAGATAA 78651 ACAATTAAAAA TATTITTTAAA AATTGGTAAAATA TACAATTAAAAAAAAAAAA
77551 TAAAATTCTG ATATACACTA CAACATGGAT GAACCTTGAA ATCTTATATAT 77661 GATGAGATGC CTAGAACAGA CAAAGGACCA ATATTATATG ATTICCACTTA 77651 GATGAGATGC CTAGAACAGA CAAATTCATA GAAACAGAAA ATAAAATAGA 77701 GGTTACCAGG AGTTTGAGAAG GAGGATAAG GAGTTATTAT TAAATGGGTT 77801 ATGGTTTGTG GACATTGATAGA GAGGAATAAG GAGTTATTAT TAAATGGGTG 77801 ATGGTTGTAG AACATTCTGA ACGTACATAG TGCACTGAA TTGTACTTAA 77851 AAGTGTTAAA ATGATTAAATT ATATTATATAT TATATTTTAC CACAATAGAA 77901 AAAAATACAA GAAGTTACCA GTGGGGAAAA GGAGGGATTA CACAATAGAA 77901 AAAAATACAA GAAGTTACCA GTGGGGAAAA GGAGGGATTA CACAATAGAA 77901 TGAAAATATG TACATACTTT CTAGTATACC TTGTTTTTGCTTATTTTACTTAA 78001 TGAAAATATG TACATACTTT CTAGTATACC TTGTTTTTTCTC TATTTTGACT 78101 ATATATCCAG ATAAATGGAAT GTAAACAAAA TACAACAAAT TAAATCTAAG 78101 ATATATCCAG ATAAATGGAAT GTAAAAAAAAA TGAAACCAAT TAATCTAAGT 78101 ATATATCCAG CAAAATTGAT ATATACCATC AGTAGAAATAT ATCCTAAGA 78101 ATATATCCAG CAAAAATTACT ATATACCATC AGTAGAAATAT ATCCTAAGA 78201 CAAGAAAGAA CAGCAAAAAAT ATCTTTAAAGT GTTTTCAGATA ATGCCATTGT 78251 TGGGGGTAAT GTTGATACTG TTATTTTAAAGT GTTTTCAGTA ATGGCATTGT 78251 TGGGGGTAAT GTTGATACTG TTATTTTAAAGT GTTTTCAGTA ATGGCATTGT 78251 TGGGGGTAAT GTTGATACTG TATATTATCAAGT GTTTTCAGTA ATGCCATTGT 78251 TTTGAATATT GTATACTGT TATATTTAAAGT GTTTTACAGT GTTTTACAGTG 78451 TTTGAATATT TATATCTAGAT GAACCAAAAAT ATCTTAAAGTAT TACTTGAAGA CCAAGAACTTGT 78301 CATTGAGAGGA AACAGAATATT TATAATGGATA ATCTTGAGAG ATTTTATATGATAGAT GTTTTACATTACA
77601 AAATGAAATA ATCCAGACAC AAAAGGACCA ATATTATATG ATTCCACITIA 77651 GATGAGATGC CTAGAACAGA CAAATTCATA GAAACAGAAA ATAAAATAGA 777701 GGTTACCAGG AGTTGGAGAG GAGGAATAAG GAGTTATTAT TAAATGGGTA 77751 TAGAGTTTTC TITAGCAATG ATGAAAATGT TCTAAAAATG GACAGTGGTA 77851 ATGGTTGTAG AACATTCTGA ACGTACATAG TGCCACTGAA TTGTACTTAA 77851 AGTGGTTAAA ATGATAAATT ATATGATATG TATATTTTAC CACAATAGAA 77901 AAAAATACAA GAAGTTACCA GTGGGGAAAA GAAGGAGATTA CAGAAGACAG 77951 GGATAACACC ACGACTTTC TCAGTATACC TTGTTTTTC ACGAAACACAG 77951 GGATAACACC ACGACTTTC TCAGTATACC TTGTTTTTC TATTTGACTT 78001 TGAAAATATG TACATACTTT ATATAACTAG AAAACAAAAT TAAATCTTAA 78101 ATATATCCAG TTTGTGGCAT AACCACACA AAATGAACTA TTACAAGTT 78101 ATATATCCAG TTTGTGGCAT AACCACCAA AAATGAACTA TTCCAAGTG 78101 ATATATCCAG AGAAATTACT ATATACCATC AGTAGAACTA ATCCCAATAGA 78201 CAAGAAAGAA CAGCAAAAAT ATCTTAAAGT GTTTTCAGTA ATGCCATTG 78251 TGGGGGTAAT GTTGATACTG TTATTTCAAA 78201 CAAGAAAGAA CAGCAAAAAT ATCTTAAAGT GTTTTCAGAT ATGCCATTG 78301 GGATAGAACC AACAAGTATT TATAATGATA TCATAGAATAT ATCCTAATAA 78251 TGGGGGTAAT GTTGATACTG TTATTTTGAA AGTGTTGAGT GTATACAGTG 78401 AAACTGAAAG CATTATTATG AAATGTGAA ATTCCTGAATG 78401 AAACTGAAAG CATTATTATG AAATGTGAA ATTCCTGAATTA 78451 TTTGAATATT TCTACAGTTA CAAGCACATA TTCTGAATGT 78501 TGTCACCCAG ATTGTCTGAA ACAGCAAATA TCCTTAATGCAG CAGACACTTA 78551 GTTTTCAATT TCTACAGTTA CAAGCATGT TCTAATGCAG CAGACACTTA 78551 ACATTATAATA TATTTTTAAACTATACA TCTAATGCAG CAGACACTTA 78501 TGTCACCCAG ATTGTCTGAA ACAGCAATAT TCCTACTGCG CAGACACTTA 78501 TGTCACCCAG ATTGTCTGAA ACAGCAATAT TCCTACTGCG CAGACACTTA 78501 CTGCACCAAAAA TAATTTTAAA ATATTTTAATAA TAATTTTAAACATAAAAAAAA
77651 GATGAGATGC CTAGAACAGA CAAATTCATA GAAACAGAAA ATAAAATTAGATA 77701 GGTTACCAGG AGTTGGAGAG GAGGAATAAG GAGTTATTAT TAAATGGTA 77751 TAGAGTTTCT GTTAGCAATG ATGAAAATGT TCTAAAAATG GACAGTGGTG 77801 ATGGTTGTAG AACATTCTGA ACGTACATAG TGCCACTGAA TTGTACTTAA 77901 AAAAATACAA GAAGTTACCA GTGGGGAAAA GGAGGGATTA CACAATAGAA 77901 AAAAATACAA GAAGTTACCA GTGGGGAAAA GGAGGGATTA CACAAGACAG 77901 AAAAATACAA GAAGTTACCA GTGGGGAAAA GGAGGGATTA CACAAGACAG 77901 TGAAAATACA CAGACTTTC TCAGATTACC TGTTTTTTCC TATTTTGACT 78001 TGAAAATATG TACATACTTT ATATAACTAG AAAACAAAAT TAAATCTAA 78051 AACAATCCCA AAAATGGAATT GTAAAACAAAA TGAAACCAAT TAATCTAGA 78101 ATATATCCAG TTTGGGCAT AACCACACAA AAATGAAATT ATATCTAAGA 78101 ATATATCCAG TTTGGGCAT AACCACACAA AAATGAAATT ATCCTAAGAG 78101 ATATATCCAG GAAAATTGAAT TATATACCATC AGTAGAAATAT ATCCTAAGAG 78101 ATATATCCAG GAAAATTGAAT TATATCAATCA ATGAACCATT ATCCAATGA 78201 CAAGAAAGAAA TACTTAAAGAT GTTTTAAAGT GTTTTCAAGTA ATGCCATTGT 78251 TGGGGGTAAT GTTGATACCT TTATTTTAAAGT GTTTTCAAGTA ATGCCATTGT 78351 CATTGAGGGA GAAGACTGAT GAAGTTAAGAA ATTTTCATAGAT GTATTACATCT 78351 CATTGAGAGGA GAGAACTGAT GAAGTTAGAA ATTTTCTATAA TCCTTGAGAA CCAAGATTTT 78401 AAACTGAAAC ATTATTATTG AAATGTGTAA TCATTGAGAA CCAAGATTTC 78501 TGTCACCCAG ATTGTCTGAA ACAGGAATAT TACAAGTTAA TCTTTAATCACA TCTTATACAGAT CTATTACACATTCC 78501 TGTCACCCAG ATTGTCTGAA ACAGGAATAT TACAAGATAA CAAGAAAAAAAAAA
77701 GGTTACCAGG AGTTGGAGAG GAGGAATAAG GAGTTATTAT TAAATGGGTA 77751 TAGAGGTTTCT GTTAGCAATG ATGAAAATGT CTAAAAATG 77801 ATGGTTGTAG AACATTCTGA ACGTACATAG TGCCACTGAA TTGTACTTAA 77801 ATGGTTGTAG AACATTCTGA ACGTACATAG TGCCACTGAA TTGTACTTAA 77801 AAAAATACAA GAAGTTACCA GTGGGGAAAA GGAGGGATTA CAGAATAGAA 77901 AAAAATACAA GAAGTTACCA GTGGGGAAAA GGAGGGATTA CAGAAAGAAA 77901 CAGAAATATG TACATACTTT ATATAACTAG AAAACAAAAT CAGAAGACAG 77951 GGATAACACC AGAACTTTT TATATAACTAG AAAACAAAAT TAAATCTTAA 78001 TAGAAATATG TACATACTTT ATATAACTAG AAAACAAAAT TAAATCTTAA 78001 TAGAAATATG TACATACTTT ATATAACTAG AAAACAAAAT TAAATCTTAA 78001 AACAATCCCA AAAATGACAT ATATACCAC CTAGTTTTC ATTTGACTT 78101 ATTATATCCAG TTTGTGGCAT AACCACACAA AAATGAACTA TAATCTAAGT 78101 ATATATCCAG TTTGTGGCAT AACCACACAA AAATGAACTA TACCTAAGAT 78201 CAAGAAAGAA CAGCAAAAAAT ATCTTAAAGT GTTTTTCAGTA TTCCAAGTAA 78201 CAAGAAAGAA CAGCAAAAAAT ATCTTAAAGT GTTTTTCAGTA ATGGCATTGT 78301 GGATAGAACC AACAAGATATT TATAATGATA TCATTGAGAA CCAAGATTTT 78351 CATTGAGGGGA GAAGACTGATG TAGAGTTAAGAA ATTTCGTAAATA 78351 CATTGAGAGGA GAAGACTGAT GAAGTTAAGAA TTTCTGAAGAT 78401 AAACTGAAAG CATTATTATG AAATGTGGA TGTGATTACC 78451 TTTGAAATAT TGTACATATA ATGATTAAC TCTATAGCAG CAGACACTTC 78501 TGTCACCCAG ATTGTCTGAA ACAGGAAATA TACAAGATAG CCAGCACATTC 78501 TGTCACCCAG ATTGTCTGAA ACAGGAAATA TACAAGATAG CCAGCACATTC 78501 GTTTTCAATAT TCTACAGTTA CATGACATATA TACATATACA CTCAACATACA 78601 CAAACAAAACA ATGATTCTACA ATGACTATATTGATT 78601 CAAACAAAACA ATGATTCTACA ATGACTATATTGATT 78701 CATTATAATA TATTTTAAGA TATATTGATT 78701 CATTATAATA TATTTTAAGA ATGACTATATT TGATTTAGAT 78701 CATTATAATA TATTTTAAGA TATATTGATT 78701 CATTATAATA TATTTTAAGA TATATTGATT 78701 CATTATAATA TATTTTAAGA TATATTGATT 78701 CATTATAATA TATTTTTAAGA TATATTGATT 78701 TAGCATCCAGA GACTTCATAGATA TATATTGATA 78701 TAGCATCCAGA GACTATCATA TATTTTATTTATTTATTTATTTATTTATTT
77751 TAGAGTTTCT GTTAGCAATG ATGANAATGT TCTAAAAATG GACAGTGTIC 77801 ATGGTTGTAG ACATTCTGA ACGTACATAG TGCCACTGAA TTGTACTTAA 77851 AGTGGTTAAA ATGATAAATT ATATGATATG TATATTTTAC CACAATAGAA 77901 AAAAATACAA GAAGTTACCA GTGGGGAAAA GGAGGGATTA CAGAAGACAG 77901 ACACAATCCAA CAGACTTTTC TCAGTATACC TTGTTTTTCG TATTTAGCTT 78001 TGAAAAATGT TACATACTTT ATATAACTAG AAAACAAAT TAAATCTTAA 78051 AACAATCCCA AAAATGGAAT GTAAAAAAAA TAAAATCTTAA 78051 AACAATCCCA AAAATGGAAT GTAAAAAAAA TAAAATCAAGT 78101 ATATATCCAG TTTGTGGCAT AACCACACAA AAATGAACTAA TTACCTATAGT 78101 ATATATCCAG TTTGTGGCAT AACCACACAA AAATGAACTAA TTACCTATAGT 78101 ATATATCCAG TTTGTGGCAT AACCACACAA AAATGAACTAA TACCTAAAGT 78201 CAAGAAAGAA CAGCAAAAATTACT TATAACTT GATGAGAATAT ATCCTAATAA 78201 CAAGAAAGAA CAGCAAAAATA TACTTTAAAGT GTTTTCAGTA ATGCCATTGT 78301 GGGATAGAACC AACAAGATTT TATATAAGTAT GTTTTCAGTA ATGCATTGT 78301 GGATAGAACC AACAAGATTT TATATATGAAT GTTTTCAGTA ATGCATTGT 78401 AAACTGAAAG CATATATTATG AAATGGTATTGAA TCTTGAAGA CCAAGAATTT 78351 CATTGAGAGG GAAGACTGAT GAAGTTAGAA ATTTCTGAAA CCAAGAATTT 78501 TGTCACCCAG ATTGTCTGAA ACCAGCAATAT TACAAGATAG ATTTCTTATACTTTACTT
77851 AGTGGTTAMA ATGATAMATT ATATGATATG TATATTTTAC CACAATAGAA 77951 AAAAATACAA GAAGTTACCA GTGGGGAAAA GGAGGGATTA CAGAAGACAG 77951 GGATAACAGC ACGACTITIC TCAGTATACC TIGITITICG TATTTTAC CACAATAGAA 77901 AAAAATACAA GAAGTTACCA GTGGGGAAAA GGAGGGATTA CAGAAGACAG 77951 GGATAACAGC ACGACTITIC TCAGTATACC TIGITITICG TATTTGACTI 78001 TGAAAATATG TACATACTTT ATATAACTAG AAAACAAAAT TAAATCTAAC 78001 AACAATCCCA AAAATGGAAT GTAAAAAAAA TGAAACCAAT TAATCCATA 78001 AACAATCCCA AAAATGGAAT GTAAAAAAAA TGAAACCAAT TAATCTAAGT 78101 ATATATCCAG TTTGTGGCAT AACCACACAA AAAAAGCAAT TAATCTAAGT 78101 ATATATCCAG GAAAATTACT ATATACCATC 78201 CAGAGAAGAC AGCAAAAAAT ACTTTAAAGT 78201 CAGAGAAGAC ACGCAAAAAT ACTTTAAAGT 78201 CAGGAGAAGAC CACACAAAAA ATCTTTTAAAGT 78251 TGGGGGTAAT GTTGATACTG TTATTTTGAA ACTGGAATAT ATGCCATGA 78301 GGATAGAACC AACAAGATAT TATATACAGT GTTTTCAGTA GTGAACATGA 78301 GGATAGAACC CACAAGAGATTT TATAATGATA ACTTGGAGA CCCAGAATTT 78351 CATTGAGGGA GAAGACTGAT GAAGTTAAGA ATTTCGATACA CCCAGAATTT 78351 TGTCACCCAG ATTGTCTGAA ACAGGAATAT ACTATAGCAG CAGACATCA 78451 TTTGAACACAA ATGATTATACA TCTATAGCAG CAGACATTA 78551 GTTTTCATAT TCTACAGTTA CAAAGCTGTC AAAACTTAACA GCCAGCAATAT 78551 GTTTTCATAT TCTACAGTTA CAAAGCTGTC AAAACTTAACA ACGACAATAT 78551 AACAAACAAA CATTATTAGA CTGAACATCA ATAAGAATAA TACAAGATAA CCCAGGAATTA 78651 AACAACAAAA CATTATTTAGA CAGGGAATAT ATCATTAGCAG CAGCAATAT 78701 CATTATAATA TATTTTTAGA AAGGGAATAT TAAGAGACAAA CCCCAGGAGTT 78801 AAGAACCAAT CATTTTGAA AAGGGTAAA TAAAGGAAAA CCCCAGGAGTT 78901 CTGGCGAAAA CAAAAAAAAA AAAAAAAAA AAAAAAAAA TAAAGGAAAA CATTAGGGT GAGATTGCCT GAGCCCAGGA GTGAAGACTCA ATAAGGAACA CATTAGAGACTCA ATAAGAATAA TAAAGGAAAA CATTAGATTAG
77851 AGTIGITIANA ATGATANATT ATATGATATG TATATTITIAC CACAATAGAA 77901 AAAAATACAA GAAGTTACCA GTGGGGAANA GGAGGGATTA CAGAAGACAG 77951 GGATAACAGC ACGACTITIC TCAGTATACC TIGITITICG TATTIGACTT 78001 TGAAAATATG TACATACTTIT ATATAACTAG AAAACAAAAT TAAATCTAAG 78101 ATATATCCAG TITGTGGCAT ACCCACAA AAATGAACAAAT TAAATCTAAGT 78101 ATATATCCAG TITGTGGCAT ACCCACAA AAATGACATA TITCCAAGTGA 78151 CITTITGAACA GAAAAATTACT ATATAACCATC AGTAGAATATA ATCCTAATAA 78201 CAAGAAAGAA CAGCAAAAAT ATCTTAAAGT GTTTTCAGTA ATGGCATTGT 78251 TGGGGGTAAT GTTGATACTG TATATACCATC AGTAGAAATAT ATCCTAAATAA 78201 CAAGAAAGAA CAGCAAAAAT ATCTTAAAGT GTTTTCAGTA ATGGCATTGT 78301 GGATAGAACC AACAAGTATT TATAATGATA TCATTGAGAA CCAAGATTTT 78351 CATTGAGGGA GAACACTGAT GAAGTTAAGA ATTTCTGAAA CCAAGATTTT 78401 AAACTGAAAG CATTATTATG AAATGGTGAA TGTGTTAAAT CTATGAGAAG 78501 TGTCACCCAG ATTGTCTGAA ACAGGAAATA TACATTACCA CAGACACTTC 78501 TGTCACCCAG ATTGTCTGAA ACAGGAAATA TACAAGATAA CCCAAGAATAT 78551 GTTTTCATAT CTACAGGTTA CAAAGCTTAC AAAACTTACT AGAGGTTATGT 78601 CAAACAAAAC ATGATCTAAC ATGACTATGT TCACAGGAAGA 78651 ACAAACAAA TCATTTTGAA AAGGGAAATA TACAACAAAC CCCAGCAATAT 78601 CATTATAAATA TATTTTTAAAG TATATTGATT GCTTTTGGAG GGTTCTAGGA 78751 AACAAACAAA TCATTTTGAA AAGGGTATA TAAAGACAAA TCACTTTAGAA 78751 AACAAACAAA TCATTTTGAA AAGGGTATA TAAAGACAAA TGACATCAA TAAGGAATGA AAAGGAAATGAA ACAGGAATGA AAAACAAAA TCATTTTGAA AAGGCACGT CATCTTACAA CCCAGGAGATT 78801 AGGACCAGTC TGAGCAACAT AATAAGAATAA TAAAAGAAAAA AAAAAAAAAA
77901 AAAAATACAA GAAGTTACCA GTGGGGAAAA GGAGGGATTA CAGAAGACAAC 77951 GGATAACAGC ACGACTITTC TCAGTATACC TIGTITTICG ATTITGACTI 78001 TGAAAATATG TACATACTIT ATATAACTAG AAAACAAAT TAAATCTTAA 78051 AACAATCCCA AAAATGGAAT GTAAAAAAAA TGAAACCAAT TAAATCTAAGT 78101 ATATATCCAG TITGTGGCAT AACCACAAA AAATGAACTAT TAATCTAAGT 78101 ATATATCCAG TITGTGGGAT AACCACCAA AAATGAACTAT TAATCTAAGT 78101 CAAGAAAGAA CAGCAAAAAT ATCTTAAAGT GTTTTCAGATA ATGCTAATAA 78201 CAAGAAAGAA CAGCAAAAAT ATCTTAAAGT GTTTTCAGAT ATGCCATATAA 78201 CAAGAAAGAA CAGCAAAAAT ATCTTAAAGT GTTTTCAGAT ATGCCATTA 78301 GGATAGAACC AACAAGTATT TATATTGATA ATGTTTGAGAT ATGCAATGT 78301 GGATAGAACC AACAAGTATT TATAATGATA TCATTGAGAG CCAAGATTTT 78351 CATTGAGGAG GAAGACTCAT TAAATGTATA TCATTGAGAA CCAAGATTTT 78401 AAACTGAAAG CATTATTATA TAAATGATA TCATTGAGAA CCAAGATTTT 78501 TGTCACCCAG ATTGTCTGAA ACAGGAAATA TACAAGAATAC TCATTAGCAG CAGCACTTC 78501 TGTCACCCAG ATTGTCTGAA ACAGGAAATA TACAAGAATAC CCAGCAACTAC 78551 GTTTTCATAT TCTACAGTTA CAAGCTGTC AAAACTTAAC AGGGTTATGT 78601 CAAACAAAAA CATGATCTAAC ATGACTATG TACAATGCAG CAGCACTTC 78651 ACATTATAAA TATTTTTAAA TAATTTAATT TCCTACTAGC G GAGCAACTA 78701 CATTATAATA TATTTTTAAA TAATTTGATT TCTACAGTT 78801 AACAACAAAA TCATTTTGAA AGTGCTAGA TAAAGAAAAA AAAAAAAAA TAATTTTAAAA TAATTTAGAA CAGGAAATAA TGACATCAAA TCACTTTGAAA 78851 ATGATGGCAC CACCTGGGTC GAGCACACTA AGTAAGACCC CATCTCTACA AAAAATTAAA 78851 ATGATGGCAC CACCTGGGTC GAGCACCAT AGTAAGACCA GAAATAAAAAAAAAA
77951 GGATAACAGC ACGACTTTTC TCAGTATACC TTGTTTTTCG TATTIGACIT 78001 TGAAAATATG TACATACTTT ATATACTAG AAAACAAAAT TAAATCTAA 78001 AACAATCCCA AAAATGGAAT GTAAAAAAA TGAAACCAAT TAATCTAGA 78101 ATATATCCAG TTTGTGGCAT ACCCACACA AAATGACTA TTCAAGTG 78101 ATATATCCAG GAAAATTACT ATATACCATC AGTAGAACCAAT TAATCTAAGT 78151 CTTTIGAACA GAAAAATTACT ATATACCATC AGTAGAAATA ATCCTAAATAA 78201 CAAGAAAGAA CAGCAAAAAT ATCTTAAAGT GTTTTCAGTA ATGGCATTGT 78201 CAGGAAAGAC AACAAGTATT TATAATGATA TCATTGAGA GTATACAGTG 78201 GGATAGAACC AACAAGTATT TATAATGATA TCATTGAGA CCAAGATTT 78301 GGATAGAACC AACAAGTATT TATAATGATA TCATTGAGAA CCAAGATTT 78301 CATTGAGAGA GAAGACTGAT GAAGTTAGA ATTTCTGTAA TCTTGAATGT 78401 AAACTGAAAG CATTATTATG AAATGGTGAA GTGTTTTAT CTTTAGATTGT 78401 AAACTGAAAG CATTATTATG AAATGGTGAA GTGTTTTATC TTAGATTTAC 78501 TGTCACCCAG ATTGTCTGAA ACAGGAAATA TACAAGATAG CCAGCAATAT 78551 GTTTTCATAT TCTACAGTTA CAAGCGAAATA TACAAGATAG CAGCAATAT 78501 TGTCACCCAG ATTGTCTGAA ACAGGAAATA TACAAGATAG CCAGCAATAT 78501 CATACAAAAA CATGAATTCAA ATAAGAATAA TACAAGATAG CCAGGAATA 78601 CAAACAAAAC ATGAACTTCAA ATAAGAATAA TACAAGATAG CCAGGAATA 78601 CAAACAAAAA TCATTTAAG TATATTGATT GCTTTTGGAG GGTTCTAGGA 78601 CATATATAATA TATTTTTAAG TATATTGATT GCTTTTGGAG GGTTCTAGGA 78601 AACAACAAAA TCATTTGAA AAGTGGTAAA TAAAGAAGAA ACTTCAAG TAGCACACATA 78801 AAGACCAGTC TGAGCAACAT AGTAAGACCC CATCTCTACA AAAAATTAAA 78801 ATATCAGCTG AGCATTGTGG TGACCAGGAG TTCAAGGACC CACTGGAGATGACT 78801 ATAGATGGCAC CACTGTGGTC CAGCCCAGGA GTTCAAGGACC CACTGGAACATAAAAAAAAAA
78001 TGAAAATATG TACATACTITI ATATAACTAG AAAACAAAAT TAAATCITAAGT 78051 AACAATCCCA AAAATGGAAT GTAAAAAAAAA TGAAACCAAT TAAATCTAAGT 78101 ATATATCCAG TITGTGGCAT AACCACCAA AAATGAACTA TITCCAAGTGA 78151 CITTITGAACA GAAAAATTACT ATATACCATC AGTAGAATAT ATTCCTAATGA 78201 CAAGAAAGAA CAGCAAAAAT ATCTTAAAGT GTITTCAGTA ATGCGAATGT 78251 TGGGGGTAAT GTGATACTG TTATTTTGAA AGTGTGAGAT ATGCGAATGT 78251 TGGGGGTAAT GTGATACTG TTATTTTGAA AGTGTGAGAA CCAAGATTT TATAATGATA TCATTGAGAA CCAAGATTT 78351 CATTGAGAAGC CAACAAGTATT TATAATGATA TCATTGAGAA CCAAGATTT 78351 CATTGAGAAG CAACAAGTATT ATAAATGATA TCATTGAAGA CCAAGATTTAC 78401 AAACTGAAAG CATTATTATG AAATGTGTGA ATTTGCTAAA CCAAGATTTAC 78401 TGTCACCCAG ATTGTCTGAA ACAGGAAATA TACAAGACAG CAGACACTTC 78501 TGTCACCCAG ATTGTCTGAA ACAGGAAATA TACAAGATAC CCAGCAACTTC 78501 TGTCACCCAG ATTGTCTGAA ACAGGAAATA TACAAGATAAC AGGGATATGT 78601 CAAACAAAAC ATGATCTAAC ATGACTATCA ATAAGAATAA TACAAGAATAA TACAAACAAAA TCATTTTAGAA ATGACTATGT TCCTACTAGG CGAGAATGA 78751 AACAAACAAA TCATTTTGAA AAGGGTAAA TGACATCAAA TCAGACATCA ATAAGAAAAA TCAATTTTAGAA ATGACTATCT TAGACATCA ATAAGAAAAA ACAAAACAAA
78051 AACAATCCCA AAAATGGAAT GTAAAAAAAAA TGAAACCAAT TAACTAAAGT 78101 ATATATCCAG TITTGGGCAT AACCACCAAA AAATGAACTA TICCAAGTGA 78201 CAAGAAAGAA GAAAATTACT ATATACCATC AGTAGAATAT ATCCTAATAA 78201 CAAGAAAGAA CAGCAAAAAAT ATCTTAAAGT GITTTCAGAT ATGGCATTGA 78251 TGGGGGTAAT GITGATACTG TTATTTTGAA AGTGTTGAGT GTATACAGTG 78301 GGATAGAACC AACAAGTATT TATATTGAAA ATGTTGAGAA CCAAGAATT 78351 CATTGAGGAA GAAGACTGAT GAAGTTAAGA TCTTTAAGAG TTATACAGTG 78301 AAACTGAAAG CATTATTATG AAATGTGTAA TCTTGAAAGT TCTTGAAATT 78351 CATTGAGAGA CATTATTTTA TAAATGATA TCTTAGACGA CAGCAATTT 78351 TGTCACCCAG ATTGTCTGAA ACAGGAAATA TCTATACAG CAGCACATTC 78501 TGTCACCCAG ATTGTCTGAA ACAGGAAATA TACAAGATAG CCAGCAATAT 78551 GTTTTCATAT TCTACAGTTA CAAGAGTAG CAACACAAAC ATGATCTAAA CAGGAAATA TACAAGATAG CAGCACATAT 78601 CAAACAAAAC ATGATCTAAC ATGACTATAT TCCTACTGC TGAAGAATGA 78651 ACATTATGAA TATTTTTAAA TATTTTTAAA TATTTTTAAA TAACTATATT TCCTACTGC TGAAGAATGA 78751 AACAAACAAA TCATTTTGAA AAGTGGTAAA TAAAGAAAAA AAAAACAAA TCATTTTGAA AAGTGGTAAA TAAAGAAAAA AAAAACAAA TCATTTTGAA AAGTGAGTAAA TAAAGAAAAA AAAAAAAA
78151 CTTTIGAACA GAAAATTACT ATATACCATC AGTAGAATAT ATCCTAATAA 78201 CAAGAAAAAAA CAGCAAAAAAT ATCTTAAAGT GTTTICAGTA ATGCATTAG 78251 TGGGGGTAAT GTTGATACTG TTATTTIGAA AGTGTTGAGT 78301 GGATAGAACC AACAAGTATT TATAATGATA TCATTGAGAA CCAAGATTT 78351 CATTGAGGGA GAAGACTGAT GAAGTTAGAA ATTTCTGTAA CTTTGAATGT 78401 AAACTGAAAG CATTATTATG AAATGTGTA TGTGTTTACC 78451 TTTGAATATG TGTATATTTA TAACTATACA TCTATAGCAG CAGACACTTC 78501 TGTCACCCAG ATTGTCTGAA ACAGGAAATA TACAAGATAG CCAGCAATAT 78551 GTTTTCATAT TCTACAGTTA CAAGGAAATA TACAAGATAG CCAGCAATAT 78551 GTTTTCATAT TCTACAGTTA CAAGAGAATA TACAAGATAG CAGCACACTTC 78501 TGTCACCCAG ATTGTCTGAA ACAGGAAATA TACAAGATAG CAGCACATTA 78551 ACATTATGAA CTGAACATCA ATAAGAATAA TGCCAGCAATAG 78651 ACATTATAATA TATTTTTAAG TATATTGATT TCCTACTGGC TGAAGAATGA 78751 AACAAACAAA TCATTTTAAG AAGTGGTAAA TGACATACAAA CCCAGGAGT 78751 AACAAACAAA TCATTTTAAG AAGTGGTAAA TAAAAGAAAA 78851 ATATCAGCTG AGCAATAT AGTACACCC CATCTTACA 78891 ATATCAGCTG AGCATTGCT TGACACAT AGTACACCC CATCTTACA 78891 ATGATGGCAC CACTGGGTC CAGCCAGGGT TAAATAGCAA GCCCCTGTT 78951 ATGATGGCAC CACTGGGTC CAGCCAGGGT TAAATAGCAA GCCCCTGTT 79001 CTGGCGAAAA AAAAAAAAAA AAAAAAAAG AAACGAATTTAAA 79001 CTGGCGAAAA AAAAAAAAAA AAAAAAAAAG AAGCACTTAAA 79051 CTATATTGAAC TGTGCCCGG AGTACACTA TAAGGAGAAA CAATACTAA 79051 CTACTGATAA AAGTACTCA GCTAAAACAT TAAGAGAAAA CAACCACTCA 79251 TGACTCAGTAA CACCACACAC AGAATACAGA CTTATTAATT 79101 CTCTGTATAA AAGTACTCCA GCTAAAACATA TAAGAGAAAA CAACAAATTAA 79201 TGACTGGATAA CACCACACAC AGAATACAGA CTTATTAATT 79351 TTACAAACTA CAACACATTC TGAACATAT AGATTGACTT 79351 TTACAAACTA ACCCACACAC AGAATACAGA CTTATTAATT 79351 TTACAAACTA CAACCACACAC AGAATACAGA CTTATTAATT 79351 TTACAAACTA ACCTAAACTT 79351 TTACAACTA ACCCCCGC CTGAGAGTTTAAT 79351 TTACAACTA ACCCCCACCACACACAC AGAATACAGA CTTATTAATT 79351 TTACAACTA ACCCCCGC CTGAGAGTTAA TAGCCTGGT CTCACCCACC 79551 TGCACCCCCG TTTCACACTA CTTACACCTAC CTCACCCTACCTACCT
78201 CAAGAAAGAA CAGCAAAAAAT ATCTTAAAGT GTTTTCAGTA ATGGCATTGT 78251 TGGGGGTAAT GTTGATACTG TTATTTTGAA AGTGTTGAGT GTATACAGTG 78301 GGATAGAACC AACAAGTATT TATATTGAA AGTGTTGAGT GTATACAGTG 78401 AAACTGAAAG CATTATTATG AAATGTGTGA TTATTTTGAAT TCTTGAAATGT 78401 AAACTGAAAG CATTATTATG AAATGTGTGA TTTTTTTTTT
78251 TGGGGGTAAT GTTGATACTG TTATATTGAA AGTGTTGAGAT GTATACAGTG 78301 GGATAGAACC AACAAGTATT TATAATGATA TCATTGAGAA CCAAGATTT 78351 CATTGAGGGA GAAGACTGAT GAAGTTAAGA ATTTCTGTAA TCTTGAATGT 78401 AAACTGAAAG CATTATTATG AAATGTGTGA TGTGTTTATC TTAGTTTACC 78451 TTTGAATATG TGTATATTTA TAACTATACA TCTATAGCAG CAGACACTTC 78501 TGTCACCCAG ATTGTCTGAA ACAGGAAATA TACAAGATAG CCAGCAATAT 78551 GTTTTCATAT TCTACAGTTA CAAAGCTGTC AAAACTTACT AGGGTTATGT 78601 CAACACAAAC ATGATCTAAC ATGACTATGT TCCTACTGGC TGAAGAATAG 78651 ACATTATGAA CTGAACATCA ATAAGAAATAA TGCACTCAAA CCCAGGAGTT 78701 CATTATAATA TATTTTTAAG TATATTGATT TCCTACTGGC TGAAGAATAG 78751 AACAACAAA TCATTTTGAA AGGGTAAAA TAACGAACACA CCCAGGAGTT 78801 AACACCAGTC TGAGCAACAT ATAAGAATAA TAAAGGAAAG ACTCAGTC 78801 AACACCAGTC TGAGCAACAT AGTACATCTT TAGTCCTAGC CACTTCAGGA 78851 ATATCAGCTG AGCATTGTGG TGTACATCTT TAGTCCTAGC CACTTGAAG 78891 ATGATGGCAC CACTGTGGTC CAGCCCAGGG TTCAAGGCT GCAGTGAACT 78901 CTGAGGGAAA AAAAAAAAAA AAAAAAAAAA 78851 ATATCAGCTG AGCATTGCCT CAGCCCAGGG TTCAAGGCT GCAGTGAACT 79001 CTGGCGAAAA AAAAAAAAAA AAAAAAAAAA 79001 CTGGCGAAAA AAAAAAAAAAA AAAAAAAAGG AAGACTTAAA CATACCTTTC 79001 CTCTGTATAA AACTACCCCACA GAATTTTGC AAGACTTTAAA CATACCTTTC 79001 TGACCTGAGTG CATACCACTA TCTGTGCAACTAA TAATTGATTA AGCACAGTTT 79101 CTCTGTATAA AACTACCCCACAC GAAATACAGA TTAATGAATA TATTATTATT AAGAGACAAA 79201 TGACCTGAGTG CATACCACTA TCTGTGAAAT AATTGATTA AGCACAGTTTC 79351 TGATCAAGTG CATACCACTA TCTGTGAAAT AATTAATT AAAGACAAT 79301 AAAAAATCTA ACCCACACAC GAAATACAGA CTTATTAATT TAATTACTCC 79451 TTTTTTTTTTT TTTTTTTTTT TTTTTTTTTTTTT
78301 GGATAGAACC AACAAGTATT TATAATGATA TCATTGAGAC CCAAGATTIT 78351 CATTGAGGGA GAAGACTGAT GAAGTTAAGA ATTCTGTAA TCTTGAATGT 78401 AAACTGAAAG CATTATTATG AAATGTTAGA ATTCTTATAC TCTTGAATGT 78401 TTTGAATATG TGTATATTATA AAATGTATACA TCTATAGCAG CAGACACTTC 78501 TGTCACCCAG ATTGTCTGAA ACAGGAAATA TACAAGATAG CCAGCAATAT 78501 GTTTTCATAT TCTACAGTTA CAAAGCTGTC AAAACTTACT AGGGTTATGT 78601 CAAACAAAAC ATGATCTACC ATGACTACC AAAACTTACT AGGGTTATGT 78601 CAAACAAAAC ATGATCTACC ATGACTATC AGAGATAG TGCACAAAAC 78651 ACATTATGAA CTGAACATCA ATAAGAATAA TGACATCAAA CCCCAGGAGTT 78701 CATTATAATA TATTTTAGA TATATTGATT GCTTTTGGAG GGTTCTAGGA 78751 AACAAACAAA TCATTTTGAA AAGTGGTAAA TAAAGGAAAG ACTTCAGTTC 78801 AAGACCAGTC TGAGCAACAT ACTAAGACCC CATCTCTACA AAAAATTAAA 78851 ATATCAGCTG AGCATTGTGG TGTACATCTT TAGTCCTAGC CACTTGAAGG 78991 CTGAGGCTG AGGATTGCCT GAGCCCAGGA GTTCAGAGCC CACTTGAGGACT 78991 ATGATGGCC CACTGTGGTC CAGCCAGGA GTTCCAGACCACACACACACACACACACACACACACACAC
78351 CATTGAGGGA GAGACTGAT GAAGTTAAGA ATTTCTGTAA TCTTGAATGT 78401 AAACTGAAAG CATTATTATG AAATGTGTGA TGTGTTTATC TTAGTTTACC 78451 TTTGAATATG TGTATATTTA TAACTATACA TCTATAGCAG CAGACACTTC 78501 TGTCACCCAG ATTGTCTGAA ACAGGAAATA TACAAGATAG CCAGCAATAT 78501 TGTCACCCAG ATTGTCTGAA ACAGGAAATA TACAAGATAG CCAGCAATAT 78501 CAAACAAAAC ATGATCTAAC ATGACTATGT TCCTACTGGC TGAAGAATGA 78651 ACATTATGAA CTGAACATCA ATAAGAATAA TGACATCAAA CCCCAGGAGTT 78701 CATTATAATA TATTTTTAAG TATATTGATT GCTTTTGGAG GGTTCAGGT 78701 CATTATAAATA TATTTTTAAG TATATTGATT GCTTTTGGAG GGTTCAGGTC 78801 AACAACAAA TCATTTTGAA AAGTGGTAAA TAAAGGAAAG ACTTCAGTTC 78801 AAGACCAGTC TGAGCAACAT AGTAAGACCC CATCTCTACA ACAAATTAAA 78851 ATATCAGCTG AGCATTGCTT GAGCCCAGGA GTTCAAGCC CATCTTACAC AAAAATTAAA 78851 ATATCAGCTG AGCATTGCTT GAGCCCAGGA GTTCAAGCC CACTTGAACT 78901 CTCAGGCGAAAA AAAAAAAAAA AAAAAAAAAG AAAAAAAA
78401 AAACTGAAAG CATTATTATG AAATGTGTGA TGTGTTATC TTAGTTACC 78451 TTTGAATATG TGTATATTTA TAACTATACA TCTATAGCAG CAGACACTTC 78501 TGTCACCCAG ATTGTCTGAA ACAGGAAATA TACAAGATAG CCAGCAATAT 78551 GTTTTCATAT TCTACAGTTA CAAAGCTGTC AAAACTTACT AGGGTTATGT 78601 CAAACAAAAC ATGATCTTAAC ATGACTATGT TCCTACTGGC TGAGAATGA 78651 ACATTATGAA CTGAACATCA ATAAGAATAA TGACCATCAAA CCCAGGAGTT 78701 CATTATAATA TATTTTTAAG TATATTGATT TGAAGAATGA 78751 AACAAACAAA TCATTTTGAA AGGTGTAAA TGACCATCAAA CCCCAGGAGTT 78801 AAGACCAGTC TGAGCAACAT AGTAAGACCC CATCTCTACA AAAAATTAAA 78851 ATATCAGCTG AGCATTGTGG TGTACACTTT TAGTCCTAGC CACTTGAGG 78901 CTGAGGCTGG AGGATTGCCT GAGCCCAGGA GTTCAAGGCT GCAGTGAACT 78901 CTGGCGAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAA
78451 TITGAATATG TGTATATITA TAACTATACA TCTATAGCAG CAGACACTITC 78501 TGTCACCCAG ATTGTCTGAA ACAGGAAAAT TACAAGATAG CCAGCAATAT 78551 GTTTTCATAT TCTACAGTTA CAAAGCTGTC AAAACTTACT AGGGTTATGT 78601 CAAACAAAAC ATGATCTAAC ATGACTATGT TCCTACTGC TGAAGAATGA 78651 ACATTATGAA CTGAACATCA ATAAGAATAA TGACATCAAA CCCAGGAGTT 78701 CATTATAATA TATTTTTAAG TATATTGATT TCTTTCAGG GGTTCTAGGA 78751 AACAAACAAA TCATTTTGAA AAGTGGTAAA TAAAGGAAAG ACTTCAGTC 78801 AAGACCAGTC TGAGCAACAT AGTACACCC 78801 ATATCAGCTG AGCATTGCCT GAGCCCAGGA GTTCAAGGC CACTTGAAGG 78901 CTGAGGCTGG AGGATTGCCT GAGCCCAGGA GTTCAAGGC CACTTGAAGG 78901 CTGAGGCTGG AGGATTGCCT CAGCCCAGGA GTTCAAGCCT CACTTGAAGG 78901 CTGAGGCTAAA AAAAAAAAAA AAAAAAAAAA 79001 CTGGGGAAAA AAAAAAAAAAA AAAAAAAAGG AACTTAAA 79101 CTCTGTATAA AAGTACTCCA GATAACTAAA TAATTGATTA AAGCAAGTTT 79101 CTCTGTATAA AAGTACTCCA GATAACTAAA TAATTGATTA AAGCAAGTTT 79101 CTCTGTATAA AAGTACTCCA GATAACTAAA TAATTGATTA AAGCAAGTTT 79101 TGACTGATAA CACCACACAC AGAATACAGA TAATTGAATTA AAGCAAGTTT 79101 TGACTGATAA CACCACACAC AGAATACAGA TAATTGATTA AAGCAAGTTT 79101 TGACTGAAGT CATACCACTA TCTGTGAAAT AATTTGATTA AAGCAAGTTT 79301 AAAAAATCTA CACCACACAC AGAATACAGA CTTATTAATT ATACTCCC 79251 TGATCAAGTG CATACCACTA TCTGTGAAAT AGTTTGACGT GAATAACTCA 79301 AAAAAAATCA CACACACAC AGAATACAGA CTTATTAATT 79301 AAAAAATCA CACACACAC AGAATACAGA CTTATTAATT 79301 TTACAAACTA CACACACC TCTAGATGTAT AGATTGACGT GACATGAAGG 79451 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
78501 TGTCACCCAG ATTGTCTGAA ACAGGAAATA TACAAGATAG CCAGCATAT 78551 GTTTTCATAT TCTACAGTTA CAAAGCTGTC AAAACTTACT AGGGTTATGT 78601 CAAACAAAAC ATGATCTAAC ATGACTATGT TCCTACTGGC TGAAGAATGA 78651 ACATTATGAA CTGAACATCA ATAAGAATAA TGACATCAAA CCCAGGAGTT 78701 CATTATAATA TATTTTTAAG TATATTGATT TCCTTACTGAG CCCAGGAGTT 78701 AACAAACAAA TCATTTTGAA AAGTGGTAAA TAAAGGAAAAG ACTTCAGGT 78801 AAGACCAGTC TGAGCAACAT AGTAAGACCC CATCTCTACA AAAAATTAAA 78851 ATAATCAGCTG AGCATTGTGG TGTACATCTT TAGTCCTAGC CACTTGAAGG 78901 CTGAGGCTGG AGGATTGCCT GAGCCAGGA GTTCAAGGCT GCAGTGAACT 78951 ATGATGGCAC CACTGTGGTC CAGCCAGGA GTCAAGCAC GCAGTGAACT 79001 CTGGCGAAAA AAAAAAAAA AAAAAAAAA AAAAAAAAG AAAAAA
78551 GTITTCATAT TCTACAGTTA CAAAGCTGTC AAAACTTACT AGGGTIATGT 78601 CAAACAAAAA ATGACTAAC ATGACTATGT TCCTACTGGC TGAAAGAATAA 78651 ACAITATGAA CTGAACATCA ATAAGAATAA TGACATCAAA CCCAGGAGTT 78701 CATTATAATA TATTITTAAG TATATTGATT GCTITTGAG GGTTCTAGGA 78751 AACAAACAAA TCATTITGAA AAGTGGTAAA TAAAGGAAAAA ACTTCAGTTC 78801 AAGACCAGTC TGAGCAACAT AGTAAGACCC CATCTCTACA AAAAATTAAA 78851 ATATCAGCTG AGCATTGTGG TGTACATCTT TAGTCCTACC AAAAAATTAAA 78851 ATATCAGCTG AGGATTGCCT GAGCCCAGGA GTTCAAGGCT GCACTTGAAGG 78901 CTGAGGCTGG AGGATTGCCT GAGCCCAGGA GTTCAAGCCT GCACTGAACT 78951 ATGATGGCAC CACTGTGGTC CAGCCAGGA GTTCAAGCCT GCACTGAACT 79001 CTGGCGAAAA AAAAAAAAA AAAAAAAAAA AAAAAAAAAA
78601 CAAACAAAAC ATGATCTAAC ATGACTATGT TCCTACTGGC TGAAGAATAGA 78651 ACATTATGAA CTGAACATCA ATAAGAATAA TGACATCAAA CCCAGGAGTT 78701 CATTATAATA TATTTITAAG TATAITGATT GCTTTTGAG GGTTCTAGAA 78751 AACAAACAAA TCATTTIGAA AAGTGGTAAA TAAAGGAAAG ACTTCAGTC 78801 AAGACCAGTC TGAGCAACAT AGTAAGACCC CATCTCTACA AAAAATTAAA 78851 ATATCAGCTG AGGATTGCGT GAGCCCAGGA GTTCAAGGCT 78901 CTGAGGCTGG AGGATTGCCT GAGCCAGGA GTTCAAGGCT 78951 ATGATGGCAC CACTGTGGTC CAGCCAGGA GTTCAAGGCT 78951 ATGATGGCAC CACTGTGGTC CAGCCAGGA GTTCAAGGCT 78901 CTGGCGAAAA AAAAAAAAA AAAAAAAGG AAGACTTAAA 79001 CTCGGCGAAAA AAAAAAAAAA AAAAAAAAGG AAGACTTAAA 79101 CTCTGTATAA AAGTACTCCA GCTAAAACAT TAATTGATTA AAGCAAGTT 79101 CTCTGTATAA AAGTACTCCA GCTAAAACAT TAAGGAGAAA TGATAGAATA 79101 TGACTGATAA CACCCCCTAAG GAATTTTGC ATCAAGACAA 79201 TGACTGATAA CACCCCCTAAG GAATTTTGC ATCAAGACAA 79201 TGACTGATAA CACCCACACA CAGAATACAGA CTTAATTAATT 79351 TTACAAACTA CACACACAC AGAATACAGA CTTAATTAATT 79351 TTACAAACTA ACCTAAACTT GAACAAGCCT CTAGATCTAA 79301 AAAAAAATCA ACCTACACAC GGAAAACAT CAGACAACA CAATAATTAA 79301 CAATCGGCAA AGTCCACACA GTGAAATAC CTAGATCTAA CACCCAATTT 79501 TGACTGGAAA AGCCCCCAGG TTCAAGTGTA AGTTTGCCA ACAAAAAAAAA 79501 TTACAAACTA CAAAGAATTG TGGAAATAC TCAGGCTAAC ATTTAGGGTC 79401 CAATCGGCAA AGTCCACCAC GTGAAAATAC TACAGCAAAC ATTTAGGGTC 79501 TTTTTTTTTT TTTTTTTTTTTTTTTTTTTTTTTTT
78651 ACATTATGAA CTGAACATCA ATAAGAATAA TGACTCAAA CCCAGGAGI 78701 CATTATAATA TATTITTAGA TATATTGATT GCTTTTGGAG GGTTCTAGGA 78751 AACAACAAA TCATTITGAA AGTGGTAAA TAAAGGAAAA ACTTCAGTTC 78801 AAGACCAGTC TGAGCAACAT AGTAAGACCC CATCTCTACA AAAAATTAAA 78851 ATATCAGCTG AGCATTGTGG TGTACATCTT TAGTCCTAGC CACTTGAAGC 78901 CTGAGGCTGG AGGATTGCCT GAGCCCAGGA GTTCAAGGCT GCAGTGGAACT 79001 CTGGCGAAAA AAAAAAAAA AAAAAAAAAA AAAAAAAAG AAAAAA
78701 CATTATAATA TATTITTAAG TATATTGATT GCTTTGGAG GGTTCTAGGA 78751 AACAAACAAA TCATTTTGAA AAGTGATAA TAAAGGAAAA ACTTCAGTTC 78801 AAGACCAGTC TGAGCAACAT AGTAAGACCC CATCTCTACA AAAAATTAAA 78851 ATATCAGCTG AGCATTGTGG TGTACATCTT TAGTCCTAGC CACTTGAAGG 78901 CTGAGGCTGG AGGATTGCCT GAGCCCAGGA GTTCAAGGCT GCAGTGAACT 78951 ATGATGGCAC CACTGTGGTC CAGCCCAGGA GTTCAAGGCT GCAGTGAACT 79001 CTGGCGAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAA
78751 AACAAACAAA TCATTITGAA AAGTGGTAAA TAAAGGAAAG ACTICAGTIC 78801 AAGACCAGTC TGAGCAACAT AGTAAGACCC CATCTCTACA AAAAATTAAA 78851 ATATCAGCTG AGCATTGTGG TGTACATCTT TAGTCCTAGC CACTTGAAGG 78901 CTGAGGCTGG AGGATTGCCT GAGCCCAGGA GTTCAAGGCT GCAGTGAACT 78951 ATGATGGCAC CACTGTGGTC CAGCCAGGA GTTCAAGGCT GCAGTGAACT 79001 CTGGCGAAAA AAAAAAAAAA AAAAAAAAG AAGACTTAAA CATACCTTTC 79051 CTATATGAAC TGTGCCTCGG AGTAACTAAA TAATTGATTA AAGCAAGTTT 79101 CTCTGTATAA AAGTACTCCA GCTAAAACAT TAAGGAGAAA TGATAGAAT 79151 CAAATATCAC AACCCCTAAG GAATTTTGC ATCAAGACAA CAATAATTAA 79201 TGACTGATAA CACCACACA AGAATACAGA CTTATTAATT 79151 CAAATATCAC AACCCCTAAG GAATTTTGC ATCAAGACAA CAATAATTAA 79201 TGACTGATAA CACCACACA TCTGGAAAT AGTTTTGCCA AAAAAAAAAA
78801 AAGACCAGTC TGAGCAACAT AGTAAGACCC CATCTCTACA AAAAATTAAA 78851 ATATCAGCTG AGCATTGTGG TGTACATCTT TAGTCCTAGC CACTTGAAGG 78901 CTGAGGCTGG AGGATTGCCT GAGCCCAGGA GTTCAAAGGCT GCAGTGAACT 78951 ATGATGGCAC CACTGTGGTC CAGCCAGGA GTTCAAAGCAT GCAGTGAACT 79001 CTGGCGAAAA AAAAAAAAAA AAAAAAAAGG AAGACTTAAA CATACCTTTC 79051 CTATATGAAC TGTGCCTCGG AGTAACACAT TAAGGAGAAA TGATAGCATT 79101 CTCTGTATAA AAGTACTCCA GCTAAAACAT TAAGGAGAAA TGATAGAATT 79151 CAAATATCAC AACCCCTAAG GAATTTTTGC ATCAAGACAA CAATAATTAA 79201 TGACTGATAA CACCACCACA AGAATACAGA CTTATTAATT GTATAACTCC 79251 TGATCAAGTG CATACCACCA AGAATACAGA CTTATTAATT GTATAACTCC 79251 TGATCAAGTG CATACCACTA TCTGTGAAAT AGTTTGCCA AAAAAAAAAA
78851 ATATCAGCTG AGCATTGTGG TGTACATCTT TAGTCCTAGC CACTIGAAGG 78901 CTGAGGGTTGG AGGATTGCCT GAGCCCAGGA GTTCAAGCT GCAGTGAACT 78951 ATGATGGCAC CACTGTGGTC CAGCCAGGAT TAAATAGCAA GACCCTGTTT 79001 CTGGCGAAAA AAAAAAAAAA AAAAAAAAGG AAGACTTAAA CATACCTTTC 79051 CTATATGAAC TGTGCCTCGG AGTAACTAAA TAATTGATTA AAGCAAGTTT 79101 CTCTGTATAA AAGTACTCCA GCTAAAACAT TAAGGAGAAA TGATAGAATT 79101 CTCTGTATAA AAGCCCCTAAG GAATTTTTGC ATCAAGACAA CAATAAATTAA 79201 TGACTGATAA CACCCACAC AGAATACAGA CTTATTAATT GTATAACTCC 79251 TGATCAAGTG CATACCACTA TCTGTGAAAAT AGTTTTGCCA AAAAAAAAAA
78901 CTGAGGCTGG AGGATTGCCT GAGCCCAGGA GTTCAAGGCT GCAGTGAACT 78951 ATGATGGCAC CACTGTGGTC CAGCCAGGAT TAAATAGCAA GACCCTGTTT 79001 CTGGCGAAAA AAAAAAAAAA AAAAAAAAGG AAGACTTAAA CATACCTTTC 79051 CTATATGAAC TGTGCCTCGG AGTAACTAAA TAATTGATTA AAGCAAGTTT 79101 CTCTGTATAA AAGTACTCCA GCTAAAACAT TAATGATAA AAGCAAGTTT 79151 CAAATATCAC AACCCCTAAG GAATTTTTGC ATCAAGACAA CAATAATAAA 79201 TGACTGATAAA CACCACACAC AGAATACAGA CTTATTAAATT GTATAACTCC 79251 TGATCAAGTG CATACCACTA TCTGTGAAAT AGTTTTGCCA AAAAAAAAAA
78951 ATGATGGCAC CACTGTGGTC CAGCCAGGGT TAAATAGCAA GACCCTGTTT 79001 CTGGCGAAAA AAAAAAAAA AAAAAAAAGA AAAAAAAGA AAGACTTAAA CATACCTTTC 79051 CTATATGAAC TGTGCCTCGG AGTAACTAAA TAATTGATTA AAGCAAGTTT 79101 CTCTGTATAA AAGTACTCCA GCTAAAACAT TAAGGAGAAA TGATAGAATT 79101 CTCTGTATAA AAGCCCCTAAG GAATTTTGC ATCAAGACAA CAATAATTAA 79201 TGACTGATAA CACCCCACAC AGAATACAGA CTTATTAATT GTATAACTCC 79251 TGATCAAGTG CATACCACTA TCTGTGAAAT AGTTTTGCCA AAAAAAAAAA
79001 CTGGCGAAAA AAAAAAAAA AAAAAAAAGG AAGACTTAAA CATACCTTTC 79051 CTATATGAAC TGTGCCTCGG AGTAACTAAA TAATTGATTA AAGCAAGTT 79101 CTCTGTATAA AAGTACTCCA GCTAAAACAT TAAGGAGAAA TGATAGAATT 79151 CAAATATCAC AACCCCTAAG GAATTTTTGC ATCAAGACAA CAATAATTAA 79201 TGACTGATAA CACCACACAC AGAATACAGA CTTATTAATT GTATAACTCC 79251 TGATCAAGTG CATACCACTA TCTGTGAAAT AGTTTGCCA AAAAAAAAAA
79051 CTATATGAAC TGTGCCTCGG AGTAACTAAA TAATTGATTA AAGCAAGTT 79101 CTCTGTATAA AAGTACTCCA GCTAAAACAT TAAGGAGAAA TGATAGAATT 79151 CAAATTATCAC AACCCCTAAG GAATTTTTGC ATCAAGACAA CAATAATTAA 79201 TGACTGATAA CACCACACAC AGAATACAGA CTTATTAATT GTATAACTCC 79251 TGATCAAGTG CATACCACTA TCTGTGAAAT AGTTTTGCCA AAAAAAAAAA
79101 CTCTGTATAA AAGTACTCCA GCTAAAACAT TAAGGAGAAA TGATAGAATT 79151 CAAATATCAC AACCCCTAAG GAATTTTTGC ATCAAGACAA CAATAAATAA 79201 TGACTGATAA CACCACACA AGAATACAGA CTTATTAATT GTATAACTCC 79251 TGATCAAGTG CATACCACTA TCTGTGAAAT AGTTTTGCCA AAAAAAAAAA
79151 CAAATATCAC AACCCCTAAG GAATTITTGC ATCAAGACAA CAATAATTAA 79201 TGACTGATAA CACCACACAC AGAATACAGA CTTATTAATT GTATAACTC 79251 TGATCAAGTG CATACCACTA TCTGTGAAAT AGTTTTGCCA AAAAAAAAAA
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79251 TGATCAAGTG CATACCACTA TCTGTGAAAT AGTTTTGCCA AAAAAAAAAA
79301 AAAAAATCTA ACCTAAACTT GAACAAGCCT CTAGATCTAA CCACCAATTI 79351 TTACAAACTA CAAAGAATTG TGGAATGTAT AGATTGACGT GACATGAAGG 79401 CAATCGGCAA AGTCCAGACT GTGAAAATAC TACAGCAAAC ATTTAGGGTC 79451 TTTTTTTCTT TTTCTTTTTTTTTTTTTTTTTTTTTT
79351 TTACAAACTA CAAAGAATTG TGGAATGTAT AGATTGACGT GACATGAAGG 79401 CAATCGGCAA AGTCCAGACT GTGAAAATAC TACAGCAAAC ATTTAGGGTC 79451 TTTTTTTCTT TTTCTTTTTTTTTTTTTTTTTTTTTT
79401 CAATCGGCAA AGTCCAGACT GTGAAAATAC TACAGCAAAC ATTTAGGGTC 79451 TITTTTTCTT TITCTTTTTTTTTTTTTTTTTTTTTTT
79451 TTTTTTCTT TTTCTTTCTT TTTTTTTTT TTTTTTTT
79501 GTCTCCCTCT GTTTCCCAGG CTAGAGTGCA GTGGTGTGAT CTCGGCTCAC 79551 TGCAACCTCC GCCGCCCAGG TTCAAGTGAT TCTCCTACCT CAGCCTCCTG 79601 AGTAGCTGAG ATTATAGGTG CGCGCCACCA TGCCCAGCTA ATTTTTGTAT 79651 TTTTAGTAGA GACGGGTTTC ACCATGTTGG TAAGCCTGGT CTCAAACTCC 79701 TGACCTCGTG ATCCACCCGC TTCAGCCTCC CAAAGTGCTG GGATTGCAGG 79751 CGTGAGCCAC TGCACCCAGC CCACCCTTGG TTTTTTTCAA CAAAAAATTA 79801 CTAGAAATAA AAGAATAATA GTTGGTCAAG GAAGCTGTAG AATAAGAAAG 79851 ACTGCCACAT ACATCAATGG CAGTGGGCGG GCTTTGTTTG AATCCAACTC 79901 TAGCATGCAA ACATTTGATA AAAATTTCTT TATTTAAAAA GAAAAGTTTA 79951 CAAAACAATC AGAAAAAATA AAAAAGATTG TAGCTCCAGTT TTATTAGATA 80001 AGCCTAGATA ATTATAAAG ATTAGATAAC TGACTCCATTT TTATTAGTTT 80051 CTTTCCTAAT AAGGCAATAT GTATTAGATA TATCAGAGTA GAAGGAAATA 80101 TTTTCTTAC ATCTATTTGG CTTTTTAAAT ATCACAACTAT TATTTTCAAA 80151 ACCAAAATGA TTTATAATCC CACCATTTAT GTAACTATCT TATTTTCAAA 80201 AAAAATTATG CAAATACTAG CATTTGTGTG CTTTTTTCC TTTTTGTGTTT 80251 GTGTGTTTAT ATCCTTTTTA AATATATCCT TTTTTATTATCC CTAAGCAGCT
79551 TGCAACCTCC GCCGCCCAGG TTCAAGTGAT TCTCCTACCT CAGCCTCCTG 79601 AGTAGCTGAG ATTATAGGTG CGCGCCACCA TGCCCAGCTA ATTTTGATA 79651 TTTTAGTAGA GACGGGTTTC ACCATGTTGG TAAGCCTGGT CTCAAACTCC 79701 TGACCTCGTG ATCCACCCGC TTCAGCCTCC CAAAGTGCTG GGATTGCAGG 79751 CGTGAGCCAC TGCACCCAGC CCACCCTTGG TTTTTTTCAA CAAAAAATTA 79801 CTAGAAATAA AAGAATAATA GTTGGTCAAG GAAGCTGTAG AATAAGAAAG 79851 ACTGCCACAT ACATCAATGG CAGTGGGCGG GCTTTGTTTG AATCCAACTC 79901 TAGCATGCAA ACATTTGATA AAAATTTCTT TATTTAAAAA GAAAAGTTTA 79951 CAAAACAATC AGAAAAAATA AAAAAGATTG AGGACTCCATT TTATTAGATT 80001 AGCCTAGATA ATTTATAAAG ATTAGATAAC TGACTCCATTT TTATTAGTTT 80051 CTTTCCTAAT AAGGCAATAT GTATTAGATA TATCAGAGTA GAAGGAAATA 80101 TTTTCTTAC ATCTATTTGG CTTTTTAAAT ATAAACATAT ATAAGTAAAA 80151 ACCAAAATGA TTTATAATCC CACCATTTAT GTAACCTATCT TATTTTCAAA 80201 AAAAATTATG CAAATACTAG CATTTGTGTG CTTTTTTCC TTTTGTGTTT 80251 GTGTGTTTAT ATCCTTTTTA AATAATCCT TTTTATTCC CTAAGCAGCT
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8U3U1 GTATACTAIA CIGCATACIA IAGIGIGAAC IIIGITCIII ICCITCATA
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80/21	AAAATTAAAA	AAAAAAAAA	GAAAAAGTTT	CACCATCATT	TCAACCTCCC
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91001	CACCAAATTA	CCATCCAGGG	ACCOUNT	CAAATCCTCT	CATACTCATA
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91251	CCTATTTCAG	TTAAAAAACA	ΔΔΔΔCΔCΔΔC	TGGTACTTTT	TITT
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81401	TGCCTCAGCC	TCCCGAGTAG	CTGGACCTAC	GGGTGCATGC	CACCACCCCC
81451	GGCTAATTTT	TTGTATTTT	AGTAGAGACA	GGGTTTCACC	ATGTTAGCCA
81501	GGATGGTCTC	GGTCTCCTGA	CCTCGTGATC	CGCCCGCCTC	GGCCTCCCAA
01551	ACTCCTCCA	TTACAGGCAT	CACCCACTGT	GCCTGGCCAC	AATGGGGTAT
01.001	TOTTLITATA	CACTCTTCAA	ATCTCCCTTT	GGAAACCATG	CCTTTCCTCT
STOOT	IGITITIAIA	GACIGIIGAA	AICIGCCIII	TACTACTAT	TAAAAATCA
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81701	ACTTCACACT	AGGTACACCT	TGAAAAATTA	TTCCAGAGCT	ATAAGAAGAG
81751	CTATAAGAAG	AAAAATATGA	TGGGTCATTG	CTCCAAAGAA	AGGTTTTAAA
81801	ΔΤGΤΔΔΔΤΤΤ	GTACTTAATG	AATAGGACAG	TGTACCCTAA	CCTCCTCCTT
91951	CCTATTCTTC	AGGGATCTCT	TCTAACAAGG	GCTAATGCTT	CACCTAAGCT
01001	CTCAAAACCC	TCCTCTCACC	ACTCCCTCTT	CAGGGTCAGA	AAAACACAAT
91301	GIGAAAAGCC	IGCIGIGAGC	ACTOCCIGIT	AATCTTCTCT	TCCTTTTCCT
81951	GAACTGTTCT	ATCATTITAG	GIICIAGGAC	AATGTTCTCT	IGCITITCCI
82001	TGCTCAGAAT	GGACCCTTGC	TGGGGTAGCA	TCAGAATGAG	GATCIGGIGC
82051	AACAGTTCTG	CAATAGGAAG	TAGGTTCCCC	TACTATCATG	GTTTTCAAGC
82101	TTTTTGACT	GCAGCCCATA	ACGAGAAATA	ATGTTTTTCA	TCATAACCCA
82151	CTACATATAC	TCACAGAGAC	ACAGTATATT	CATAAAAAAA	ATCATAACGT
02111	TTAACCTTAT		TTTATCCTAT	GTTATTCAAT	CTATTTTATT
02201	TIAACCIIAI	GITAATAGCA	CACACTTAAC	TAAACTCATT	TCACAACTCC
82251	TCTTTTAAA	AAAIGCICAI	CACAGITAAC	TAAACTGATT	TACAACTCC
82301	TTAAAGGAAT	TTGACTCACA	ATTTGAAAAA	CACTGCATTG	IAGAATATT
82351	TAGAGTCTCT	TCCCAACCCT	CAGAGTCAGA	TTTATTTCAA	GATGGCCCCT
82401	GTAAGACAGC	TTCAAGCTTG	TGAGTGACTT	тстттттст	TTTTACTTCT
82451	TTACCATITA	CCATGACTCC	CAAATAAGTG	ACTCTTTTGG	CTTATTTGGT
92501	AACCATGCTA	ATTTCTACAC	ΑΤΛΓΑΛΙΟΤΑ	GAGCATTTAC	<b>ΔΤΔΔGACCCA</b>
02301	CCCAAACCTT	CTCTTTTAAC	CTTCCTTCTC	TCCTTTCTTT	CTITCATTCA
02221	CCCAAAGCII	GIGITITAAC	TATCTCTTCA	ATCTCTCTT	CACCCACTCT
82601	. IIGALIAIGI	TITCIATIGO	IAICIGIICA	ATCTGTGTTT	CAGGCAGIGI
82651	. ACAGGTACTG	AGGCAACAAT	GGTGAGTAAA	AGCAAGCATG	CATCCTGAGA
82701	. TATACTGGGA	ATGAAAGAAG	CTAATCCAAA	. AGCATACAGG	AAAATATTTT
82751	CAAACTTTGA	TAAATTCTGT	GTAAGCATAT	GGCATTGCAC	GTAACAGGGG
82801	AACCGCATTT	AATATGGAGT	GTTGGAAAAG	GCTTCTGTGA	GAAGTGACAC
82851	TTGAGCTAAG	ACTAGAAAAG	TGAAAAGAAT	ΔΤΔΔCCΔGGT	ACTGGACAGC
02011	ATCATCACTO	CACCCACACC	TCACATCCTA	TCACAACCTT	CTAAGGCTGA
82901	. AICAIGAGIG	CAGGCACAGG	TGACATCGTA	1 CACAAGCT1	TOTTCAACAT
82951	. AGGGGGCGTG	AATIGCIAGC	. IGGAGAGIGG	AAGGAAAAGA	TCTTCAAGAT
83001	. AAAGCTGGAA	. AAATAAACAG	GGCCAGGCCT	CATAGGTTTC	TGTAGACCAT
83051	. GGAAAGAGGT	GAAGGTTATT	TTGAGCCTGG	<b>ATGACATGAT</b>	AAAACTCACA
83101	TTGTAAAAAT	ATAACTGCAA	GGTAGAGAAT	GGATTGAAGA	GGTCCAAGAT
83151	TACGCAGACA	GAGCTATGAA	CAGCCTATTO	CAATGGTCTG	GGTCAAGCAT
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02701	TACTCACCAC	ACTTTCCA	CAATTCAAA	TECACTOCCA	CCAGACTTGT
82727	LIACIGAGCAC	. ACTITICAAT	GAATIICAAA	TAACCO	CCAGACTTGT
83301	L TAATTITGGA	GCIGTCGACT	AACAAATAAG	IAAGCCAIGA	TAACCCACCA
83351	L AAGAAAGTTC	<b>CAGAAATGCA</b>	\ AGAGCAAGG(	: TGTGATGAAT	GGTTGAGGTA
83401	L CAAGGAAGCT	CTTACTCACT	CATTTTAAAA	A AATCAGATGA	TATGAAGTTG
83451	ΑΑΤΑΤΤΟΔΔΟ	ATATTGCCCA	ATTGTGTTAT	GTTCACATAT	TTTACTGGGC
82501	ATACTTCTCC	ΑΤΔΔΤΛΛΛΛ	ΔΤΤΤΔΤΟΤΤ	TCTCCCTCTC	AGAATTAAAA
02561	L AIAGIICIGO	, ~!~~!~~~\	ATCTCCCAAA		GATTTTTAAG
03337	LAICIGAGAIG	COCTOCATO	TTAAATACAT	TTATATTTCT	ACTCCCCAAC
6360	L AGCCAAACGT	GCCTCCATGA	TIAAATACAT	TOTOTOTO	ACTGGCCAAG
83651	l gaaagcatgt	rgcctcttgc	. CIGGGCCTC	ICIGICITO	ATTAATAATC

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- 44CA4
- 4.654
- 65454 66646 <del>77</del> 664 6776671611 1661146111 11100110071 0071001111
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80/31 IAAAGCIATA GAGATATAC AGAGASTES

86801 AATTIGTAGT TICAATGATG ATTITATATA TAGTATCTCA TITGATCTCT
00001 CAAATAACCT CACATAAATC AII QGQGLQG AG ALAIMAIIAQ AGIAGCTIII
ACAA1 AATATCAAAA AATCATCCCT IGIAIAGAII AAAIIAICAC CCAGIIIAC
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87001 AAAACAACTA GTGTTTACTG GTTGATAAA TCCTCAAAAC TCAGCAAAGA 87051 TAGGTACTTT ATGTACATTA GTTTATAAA TCCTCAAAAC TCAGCAAAAGA AAACTGTCTC
87051 TAGGTACTTT ATGTACATTA GTTTATTAC ACAGATAAAG AAACTGTCTC 87101 TTCCACATTT CATTATAATA TTCCCATTAC ACAGATAAAG AAACTGTCTC
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87151 AAAGGTTTGC CAAGGACAAA AAAGTCAGAA TTCTATGATA CCAATTCACA 87201 ACCTAGATCT CTCTGACCTC AAAGTCAGAA TTCTATGATA CCAATTCACA
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OFFICE ATTECETICAC ATTITANGTA (AALIAIGIL ILAAIIAGIA AAAAGIIOO
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87851 ACACCIGGIG TITTITICAA TAACTATA GCTCTTTCTG AAGAGAGACT 87901 CTTCCCATAC TGGTTTTCTG GTCCCTCATA GCTCTTTCTG AAGAGAGACT
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88651 CCTGAGGAGT TOTAGACATT GOTTTTGCTTT TCATTGTATA ACCAGTATGT
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0/751 TECTTAGGA AATECCETTT CTTTTTGTTT TGGTAAATCI ICIIIICAGI
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OSONI TITTACTITE CCCAGAATAC ATTATAATAT AAAGCIIAAG CIIIAIICII
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OSOSI CCAAACATTA AGAAAGAACA ATAATCTTAC TAAAAAGCAG AGIGIGGIAI
OGOOT GCTAGAGAGA TTAAGAGGCT TTGGAATAGT TACATCAGGG ATCAATTAGT
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OCOEL ACCATACGAA ATTAGAAGTG AGGAGTAAII IGGAGACIGA CAAGCICIAC
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OPONI TTANCATEGE TETETITIT GAGACCAATA GUULATUIGI GACACCUTAA
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- 4 6 2 E 6 4 - 6 6 6 F C C 6 A F - T T C T C T C C C C C C C C C C C C C
- 400004
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4 A E A E 4 - A-C-T-T-CA A A - T-C-A A-T-T-A A-C - 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
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TOOOT	CITACIGACI	CATATICITI	ATATTCATCT	GAAAAAATT	CTTCTACATC
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		GGCCAGCACT			
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1114UJ	COACCACCA	· ~~!~~~~!\\	. 10010A1AAA	- CAAACAACTT	TEATACACCC
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113501 GAAAACTTAC TTCGTGTTCAA TAAATACCTA CTAACTGTCT CTGTGTGCTT 113551 AAAAATATTA ACTAATTCAA TAAATACCTA CTAACCAACA CAGACAAGGT
113531 AAAAATATTA ACTATICCGG TGACCCTGTA GAAAGCAACA CAGACAAGGT 113601 AGCACTGTTT CAGATGCCGG TGACCCTGTA GAAAGCAACA CAGACAAGGT
113601 AGCACTGTTT CAGATGCCGG TATCTAGTGG GAGCAGATTT ATAAAAAAAA 113651 CTTCAGATCC TGGAGCTTAC ATTCTAGTGG GAGCAGATTT ATAAAAAAAA 113701 AAGAACCAAA CAAGGCCGGG CATGGTGGCT CACGCCTGTA ATCCCAGCAC 113701 AAGAACCAAA CAAGGCCGGG CATGGTGGCT CACAAAAGAT TGAGACCATC
113701 AAGAACCAAA CAAGGCCGGG CATGGTGGCT CACGGCAAAAGAT TGAGACCATC 113751 TTTGGGAGGC TGAAGTAGGC AGATCATGAG TAAAAAAAAAA
AARONA GTCCCCAACA TCCTCAAACC CTGTCTCTCTAAAAAAAAAA
4430F4 CCCTCTCCTX CCXTCCCCCC
442001 CCACAATCCC TTCAATCTCC CACGGGGGGGGGGGGGG
1120E1 CCCATTCCAC TCCACCCTGG (GALAAGGG AGALIICUIC ICCCCCCC
444001 CAAACAAACA AACAAACAAACAAA GAAGIAGGAA ALAGIAAIAA QQOOOOO QOO
- 44 40P4
- 11/101 CATACATACA CCTATAAACT TIACAAAAIA LAIILLLAUL IMIGOTIIIO
444464 CATTELET TACTCETACA ALBAILLE AL GARLICI DI CITATONIO
44 ADOL AACCAAATTC TCCACCTCGA TGGTGGCAIG CAICTUIG CCCAGCTGC
44 43 E4
114301 CTCACCTATC ATCATCCCAC TGIACICIAG CCIGAGIGAI AAAGIGAGA
444364 TCTCTCTCTX XXXXCXXXIX AAIIAIIIII AAAAAIAAAI 777799999
11/4/01 AAATTCTCCC TCAGAAAGTT 14441G1C11 16CA11A111 1616161799
1144E1 CACCTCACCA ACTCGTTTTT GCCTIGALAA IILAGCATTI ACTAAGGGG
A A A COAL CACCAAAAAC ACACTCTTAC A HOLDADAH GILAGII GULAGII GULAGII GILAGII GILAGII GILAGII GILAGII GILAGII GILAGII GILAGII GULAGII GILAGII GI
A A E E A CONTROL CANATONACT NONABACTIC LABORITORIO
11 ACO1 ACCCATCTAT ATACACACCA GAALIAGIIG IIAGCAGAAC CAGCIIIACI
114601 AGCCATCTAT ATAGACACAAT GCAAGGAGAG AGCTAGTGTC CTCGAGGGGGG

114701 CACACAGTAT TCAGAAAGAG GGAGTTCTCC CTCCCTTTTC CCTGTGGTTG
44.4664 A.A.C.C.C.C.C.C.C.C.C.C.C.C.C.C.C.C.C.C
44 ACE4 CTCTACTTAC TCCACTIC-IC ACTICALL IN MANITACION COCCIONII
AAAAAA AACAACAAAAAAAAAAAAAAAAAAAAAAAAA
-445004 6766477466 TACACCCII. I GAILLALLI CALAIDUME ESISSIII -
-44 FOR4 - 664 A CA A TAT - A C C C T C C A A C - (4-A (-4-(-4-(-4-(-4-(-4-(-4-(-4-(-4-(-4-(-4
AARAAA AAAAAAAAAAAAA CAAACTAAAAAAAA INGAGOO OO
-44 E4 E4 -466 ACTOTAC CCATACTCTC ALLIADAGE I CILAGCULAD IICCICCII
-44 ESE4 - 464 CCCTACC ACATCTCTCA (-(-ALLLILL IIII IIIIIIIIIIIII CCC)
115451 ATTCACAGAA CTGAATTGTA AACAGACTGA GATATCATTA GGCGAGCTCC 115501 AGGACTAAAA CTTATTAGGC AACAGACTGA GATATCATTA GGCGAGCTCC
115501 AGGACTAAAA CTTATTAGGA ACCAGACACT GCACAGTTGC TGTCAAATGA 115551 TTATCCAGCA AAAACAGGAA GTTAGACACT GCACAGTTGC TGTCAAATGA
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115651 GTAATCCCAG CACTTIGGGA GACCGAGGGA ACCCCATCTC TACTAAAAAT 115701 GATCGAGACC AGCCTGGCCA ACATGGTGAA ACCCCATCTC TACTAAAAAT
115701 GATCGAGACC AGCCTGGCCA ACATGGTGCA TCTGTAGTCA TAGCTACTCG 115751 ACAAAAATTA GCTGGGCATG GTGGCGTGCA TCTGTAGTCA TAGCTACTCG
44=664
115801 GGAGGCTGAG GCAGGAAAAT CACTTCCAGCC TGGCGACAGA GTGAGACTCC 115851 GAGCCGAGAC TGTGTCACTG CACTCCAGCC TGGCGACAGA GTGAGACTCC
AARARAACCCTAA TTACTTAACA TGC CLAAAGC AGGIGGAIGIG GIGAIGIG
44CAA4 #C##FAAACT CCTCCCAIIA AGII (4131411311 AAIUAAIIU) II UVUUNIN
- 44 C4 A4
446364 66764677776 CAACACAAAT (
- 44 CO E4
AACOOA GCCCCAATAA ATCTCTTTIG ILALIULAA AALAALUUMU MIMIMIMI
446464 ATCCAACCCT CCTCCTCTCTCA
44 CAPA
AACEGACCACCCT TCCTTTCCAT (-[-1]-AGAGAAA GTALUUUUAG UCCACCTTTC
44 CEE4
44CCO4 TCAAACTTCC CATTTCTAGI ( ) I ( I LALAA GA HAGAACIA GOTTO )
116651 ACCTAGGAAA AATTCTGTGC ACCTTCCCTGG ACCAGACAAG GTGTTAAATG 116701 TGACTAATAT TTCTTGAAAT CTTTCCCTGG ACCAGACAAG GTGTTAAATG
116701 IGACTAATAT TICTIGAAAT CITCECT CAGCAGCCCC ATGGGGTGGA 116751 TTTTACATTC ATTTATTTGT TTATTTTTCT CAGCAGCCCC ATGGGGTGGA 116801 CTATACTTAT CACTACTTTA TAATGGGAAAA ATCAGAAGC TAAATAATTT
- 446084 AARAAAAATA TATATIIGIN NAIAIIIIA ICIGIGGIII III IIIVVVIVOSII
443344
449464 64466446CT TTTC/TTTTT
117651 CTCTACTAAA AAAAATACAC AAAAAATTACAC AAAAAATTACAC AAAAAAATTACAC AAAAAATTACAC AAAAAATTACAC AAAAAATTACAC AAAAAATTACAC AAAAAAATTACAC AAAAAATTACAC AAAAAATTACAC AAAAAATTACAC AAAAAAATTACAC AAAAAATTACAC AAAAAAATTACAC AAAAAAAA
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117801 TGGGCGACAG AGCGAGATTC CGTCTCAAAA AAAATAAAAT
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119501 GATATIACCA CAGIATITCI IIGAGITETTA TACTITITATO CTATICCAAT 119551 ITCTITGCTC ATTITCTATT AAGGITGTTAA TACTITITATO CTATICGAATA
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440004
4400P4
- 4400P4
4300E1 AATATOTATA TTOTOTAGAL LILAAALUIL GIAGGIIIOI OOOIIVVIIIO
490404 ATCCCATCCC CCALLETTE TILATION INCOMPONIUM TOURS TO THE
455564 4477447766 ATTAAATCTA IAGAIIAGIG IIGGILLULI IIGIGIL
ADDIE COTORO ATTIANIAL LALGILIANA AMMALUIDO COSTO INTERPORTATION
400004 -004447664 AATATTTAAL AAALALA AAALALAALA AAALA
ASSET OF A ACADEA CANTECENAT LINDALLALA GIUAMAIACI ALICOCOCO
400E04 4464CTTTCC TAAATACTII (-(-A(-)IIA) II IIIIIACACAU AVVVVIIIVY
455664 -66666TTATA CCAATACTCA [AIGHALAHAHA AACHH CAID ACACCAIII
ASSOCIA TOLOLOTO CONTRACT CONTRACTOR AND
120801 GAAAAGTAAG ACACCAAAGA ATACAAGGA GGCATAGATT TTTTTTTGCT 120851 TTTAATTTAA TGGAATTTAA TAGAATACAA GGCATAGATT TTTTTTTGCT
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120901	TTGTTAGTGT	TTCCTTTATT	ATAAAGCACT	GAAATAAATA	AATAGGTAGC
120051	TACCCAATTT	<b>ATCCACAGTT</b>	TCTGGGAGCT	ATATAAGATA	GGCAAAGCTA
121001	AACTATTGTC	ΤΔΔΔΔΔΤΑΤΩ	TACATAGATA	TTGATCTATA	TAGAAAAACA
121001	ACAAAATTAT	ΤΛΛΓΛΤΛΛΛΛ	TTTAGCACAG	TGACTTCTAG	GGTTATGAAC
121001	ACAACACCAC	ACACTGATGG	GGACAAGATT	CTATTTCTTG	ACCTGTATCA
151101	AGAACAGGAC	CACATTTCCT	TATAACTGTT	TECTAATTET	GCAGTGTTTT
121121	IGITIAIGIG	GACATTIGCT	CTATACAAAT	ACATAATCAC	CAATACCAAA
121201	ATTTACTTT	CIGAATATAT	GTATAGAAAT	CTTACCCCTT	CTCTCACTCT
121251	CAAAATACTC	AGTGGCTTTT	TTGAAGGACA	CTTAGCCCTT	TOCTCALACC
121301	CTTAGTACTC	TCTTAGGTGC	AGGGAATCTT	CTGGAAGGGI	IGGIGAAAGC
121251	CCTTCAATAT	CTTCCTGCTC	TGGTTTCTCA	GCTAIIIGAG	GGCTCAAATA
121/101	ATTACTCGTC	TGTTATGTTT	TTGTATGTTG	ICATAAGGII	ICHICHAAI
121451	GTTCCACCAA	AATGCTTCAG	TGCCTTGCAT	ACCATGAATA	TTTTCTGAAT
121501	GAATAAATGT	GTATTAAAAT	GTTTTAATGC	CTGAAAATAG	ACCAGGTAGA
121551	ACACCATGAA	ΔΔΔGΔΔΤΑCΤ	GGATAAATAA	AGCTGGAAGA	AAGAAAGAAA
121501	CTCAAAAGAA	TACTCATGTA	AACCCCAAGG	ATAATCCAAT	ATGACAGATA
121001	CATAACTTCT	ATACACTAAT	GTTTATTCTA	TTAGGCATTT	TCTTAGCACA
151001	CATAACTIGI	TTATCCCTCA	AAGTTCTTTG	TACCTTCTCT	GAGTGACGTG
151/01	GIGGCICIGA	ATCACCTCC	CACTATCTCA	TATEACTTET	TGTGAGATAC
121/51	TCTGTCACCC	ATCACCIGGG	GACTATCTGA	CTCTCTCTCC	CACTACTCTC
121801	TGAGAAGGGA	GAGCAGAAAI	ATAGTCCATC	TOCCOCCTCT	CACTTCCACA
121851	GGGTCAGGGC	CATTACCTCC	CAAATTGCAC	I GGGGGCTGT	ATACCCCTCC
121901	AAGGATGCAG	TGATTCATGA	AAGGTGAATG	CACTAGGGAA	ATAGCCCTCC
121951	TTATTCCTGC	TGCATCAAGC	TCTTATAGTC	AGGGCCAGTC	CCGGGCATIG
122001	GGATGTAAAC	ACTCTACCTC	TCTAGTTGGA	TGTTGTTCAC	AGGATITIAC
122051	ΤΤΔΔΔΔΔGΔΔ	CATGAGTGCA	CTGGGTAGGG	AAAACCIGIG	IGIGCAGGAC
122101	CCATGTCATA	CCAGTTTCCT	TTGCCCAGAG	CCAGCACTII	ATACAGGAGG
122151	CTTGGGATCA	<b>ACCATACAAA</b>	TCTTTCAACT	AGGTCAATTA	TIAIGAAIGI
122201	TTGCCTCTCT	AGAAGCCTAC	CCAATGTTTC	TGAGCACTIT	ATAAGTGCTA
122251	GGCACCATAC	TGAGATTTTG	ACATGGATTA	TCACTGIIAA	HILLIAACIC
122201	TATAAAGATT	GCCTTATTGG	CTGGGTGCAG	TGACTCACAC	CIGIAAICCC
122301	ACTACTTTAG	GAGGCCAAAG	CAGGTGGATC	ACCTAAGCCC	AGGAGTTCAA
122331	CACCACTCTG	GGCAACATGG	CAAGACCCTA	TCTCTACAAA	AAGCACAAAA
122401	ATTITACCAA	ATGTGGTGGT	ACCCACCTGT	AGTCCCAGCT	ACTTGGGAGG
122471	CCAACCTTCC	ACCATCACTT	GAGTCTGGGA	GGTCGAGGCT	GCAGTGAGCC
122301	ATCATTCTAT	CACTGCAATC	CAGCCTGGGC	AATGGAGTGA	GATTCTGTCT
122601	. AIGALIGIAI	4444444	ΔΑΔΑΔΑΔΑΘ	AAAGAAAGAA	AGAAAGAAAA
122601	. CAAAAAAAAA	C	AGATTGCCTT	ATTGTTCTGC	TTTTGCTGTT
122201	. AAAAGGAAAA	TCCCAACTTC	CTCAAGGTCA	CAGTAAGTGG	TGAAGGTAGA
122701	. ICICAGGCIC	ACACACCACA	CCTCCAGAGC	TAATGATCAC	AACTATTGCT
122/21	. ATTIGAACCC	AGAGAGCACA	TCATTCAACA	AATTTCTCTC	CAGTGATTCT
155801	IGAGCAATIG	ATTIGITCAT	CACACTACCA	ATATECTECT	GAGCATGCAG
122851	. GAATGCCAGA	TOCCTATIO	GACAGIAGGA	TTCTCCCTAT	GAGCATGCAG
122901	L AAGCATICCC	. IGCCIIIGCI	CAACCCTAAC	TAAAACCTTC	TACATCCCTC
12295	. AGGAGTTAGG	TTIALICITA	GAAGGGTAAG	CCTCTCTCCC	ATAGTGTGTC
123003	L AAAGTGCTTA	GAGAATGCAT	AACIIGGGGI	CCICICIOGO	GGTAAAATTG
123051	L ACTGTAGCT	TGCCTTCCAC	TGGAATCAAT	IGAAAGAACI	ACAGTTACAA
123101	L AGTGTAAAGA	ACCCACAGCT	GTTGTAAAAC	. CITACACICI	CCAGAATGCT
12315	L TGCTCCCTC1	тттстссст	CCTCATCCCC	AACAGATGGC	TGCAAGTGCT
12320	L TCCCTTGCT(	CTTCCAGGT	ACTCTGAGAT	AGAGAGATTA	TCCAATGTAT
12325	L GCTGTACCA/	A ATTCTGCACO	S TTGTCTGCGA	CTGTTATAGA	AATTTAGATC
12330	L CTTTAGTTGA	A AACCTTCCC/	A ATCAAAACAA	ATAACATCTI	CTTAGCCTTC
12225	1 TTGATTTCAC	: GGTGAGCCA(	C ATATTTGAGO	: CCCAATAGGA	CCCAAATITI
12340	1 AATCGGTGCA	A TGATCTAAA?	Γ AAGCGAAGA(	TTTATCCATO	AAGGCCIAIG
12345	1 CATGCCTGTC	TGTGTTGAC	r gatgaatga0	GCTACTGAGA	GAGATTAGAA
12350	1 ΔΑΤΤΔGΔΔΔ	r GTTTGCCTG(	TGTGAGCAA	r CTAGCAACG	AIGAIAAACA
12255	1 ΤΓΓΑΤΔΔΔΔ	; TGTTTATAT	r TTTGATCCT0	GTAATTCIC	, IIIGGAGGAA
12360	1 CATGTTGAG	Α ΔΔΑΤΑΤΑΑΤ	A CTAATGTCT	: AGGGAATCAA	A ACIGGIIIAA
12365	1 TTTTTCGTG	r TTTTCAGCAG	C CTGAGATGT	F CAGCTCCAGA	AAAGGAGCAG
12270	1 CCTATTCCT	r TGCTGTTGAG	c TGGTGGTCC	TGGGAGTGAG	, GGCATATGAA
17275	1 CTCCTGAGAG	s GCCGGGTAC	T GTAGTAGCA	r ticciciii	GHAIIIIC
12200	1 CACCAACTT	C TATTTACA	A TGAAAGAAT	TATTGTTTG	TAAGATCCAA
1220F	1 CAGCAAGII	T TEANACETE	Δ ΔΔΤΓΔΩΓΤΔ	T GCCATGTGAT	GTTGATAACA
12200	1 CCCCTTCAC	, IGAAAGCIG/ A TTTCTCCAT	A GGTTAATTC	A TTTGTCCCG	ATATGGGACC
12205	1 AACCATCTC	A TITCIGUALA	Δ ΔΔΤΤΔΛΑΓΟ	G TTAAAAGTAA	A AGGAATAATA
17333	I AACCAIGIC	A ALIACCALL	~ ~~~~~~		

124001	TGGATATTAT	AAACTCCCAA	AGAGGGGAAA	TCAATACACC	TCACTAAATA
124051	TCTTGTGTAA	ATATCTGTGT	TTGTTTAAAG	AAAGTCATTT	TGCAGTCATA
124101	GTACAGGACT	CTAATTCAGA	CATACCTCAC	CAAGGCTAGT	GTGAATTATT
				<b>GGATTTCTAT</b>	
				TCATTTCCTT	
				AAAAAAGAGA	
				TTGTGCAAAC	
124351	TAGAAATACA	CTCCTTAGGT	TATATCTCAG	TCAGCTCTGC	TTACCATAAT
124401	AAAATACTGC	AGACAGGATG	<b>GCTTAAATAA</b>	CAGACATCTA	TTTTCTTGGT
				CCAGAATGGT	
				ССТТТТТСТ	
				AGTCTACTAA	
				CTTATTCCCT	
				AAGGCTTCAA	
				CATTCTATCC	
124751	CAATATTCAT	GTCCTTCTCA	TATGCAAAAT	ACATACATTC	AACAGTCCCA
124801	AAAGTCTTAA	CTTATTCCCA	TATCAACTCT	AAAGTCTGAA	GTCCAAAATC
124851	TCATCTAAAC	ATCATAGAAA	TTGTGTATGG	GTGAGACTCG	AGGTATGATT
124901	CATCCTAAGG	CAAAATTTCT	CCTCAGCTAT	<b>GTACCTATAA</b>	AAGCAGACAA
				CCAACACTTT	
				TGAGACCAGC	
				TTTTTAATTA	
				GGTGGTTGAG	
				GAGCCAAGAT	
				CATCATTAAA	
125251	CAAAAAACAA	ACAAACAAAA	AACAAGCAAG	TTATGTGCTT	CCAAAATACA
125301	<b>ATGATACCAT</b>	AGCTGTGGGA	TAGAGAATCC	CATTCCAACA	TTTCAAAAGA
		AGAAGGAAGG			TCCAGAACAT
		ATTCTATTAT			TCTTCTTTGA
				GCATGGGAGC	
		ATGGGGAGAG			TCTACAAAGG
				TGTCTACACA	
				GAGGCAACCC	TGCTCCCCAA
125651	GCCAGTGCAC	TCTGGACCTG	TAGTGGGAAT	GGCAGCCCTG	ATGATCTGTG
125701	AATCGCCCTC	ATGATCCTTC	TTCCTTTTAC	TTGAAGGATA	GCACATGTTC
125751	ACAGCTGGAT	AGCATTACGG	TCCCAGCCTG	TAAAATCCAA	GAAGTCTGAC
				ATCTGCTAGT	
				CTTGATTGTT	
				TTTTCTGCAA	
		TTCTGGTTGC			CTTCAATTCA
				GACAGAAGGA	
				GGCTGGCCTG	GTGCAGTGGC
		AATCCCAGCA			CAGATCACCT
126151	GAGGTCAGTA	ATTCGAGTCC	AACCTGATCA	ACATGGAGAA	ACCCCATCTG
126201	TACTAAAAAT	ACAAAATTAG	CCGGGCATGG	TGGTGGATGC	CTGTAATCCC
				ACTTGAACCT	
				ACTCCAGCCT	
				AAAAAAGAAA	
				TACCTTCTGC	
				TATAACAAGA	
				CTGTCAGACC	
				CATCCACAGT	
				TTAAGGCATT	
126651	GCATTCCAAT	TCTCAATACC	AAAATTTTAG	TCTGCAATAT	CTGCCTTCAC
126701	AAAATACCAC	AGAATTGGTG	GCTTAGGCAA	CAGAAATTTA	TTTTCTCAGT
				CCATCATGGT	
				TTCTTTCTTG	
				TTTTGTAATA	
				TAATCTAACC	
				ATTGAAGGTT	
					TGTATACTCT
127051	CAAGGTCCCA	GTGATGGATG	CAATCAGTGA	TTCCTCTAAG	ACCAAAGAGT

127101	TGAAGACCTG	ACTTTAGGAG	CTTGTTTATC	CCACAGAACT	AAAGAATTGG
127151	GTATCTCAAG	TCATCATCCA	GATACTGCAG	CTCTCCTCTC	CTAACTITTT
127201	GGAGTCATTC	TTTCTCCTCC	TETCAATAGE	CCTCTTCTTT	GGTCCCACAA
12/201	GUAGICATIC	TOATTTOTOG	ATTAAAAATC	CCATCTCCCA	ACTAATTAAC
T5/52T	CACACCATCA	IGATITICIGE	ATTAAAAATG	CCATCTCCCA	AGIAATIAAC
127301	CTATTCACAG	TAAGAACAGT	TGTTAGAAGT	TGGGGTTATT	ICATCATGGT
127351	CCAATGGCTT	TATCTTGCTC	AGGAAATCAA	AGATGAGTGT	TTCTAAAGCA
127401	AAAAAAAGGA	GGATCTCACA	ATTGTATCTG	TTTCATTCAC	TCTGCAGGGT
127/51	CCATTTTACA	CCCAAACATT	CATTAGTTCA	TTGTTTGTAC	TCCTGCCTTT
127501	CCTGAGGAAG	TCATTCTACC	ACTATTTCTT	AACTATATTC	AAATTTGGAT
15/201	CCTGAGGAAG	ICATIGIAGE	ACIAITICIT	COTTOTALCO	CAAATCTCTA
127551	AAGTTAGTCA	AATTGATGTG	AAAGGACCAC	CCTTGTAAGC	CAAAIGIGIA
127601	<b>AGTCCTACAT</b>	AGGGATATTA	CCTGTTTTTA	TCTCCTGATG	GGCTTTTTTT
127651	TTTTCAAGTT	TCTAAATAAA	TCCAGTGAAC	AAGTAGATAC	GCTACTCATG
127701	<b>ATTATATAGG</b>	ΔΔΔΔCΔGΔGΔ	AGAGAAACAT	ACACTTACTT	AAAAGTAGAA
127751	ACATATCTGC	TCTTTCCCAC	TTCACCCTTA	ATTITUCT	CCCCAGCCAA
127701	TTTACTCACC	TTCTCTCCCT	CTCCTTCTCT	CTTAGACCCT	TECTACCTEC
12/001	TTTACTCACC	TICIGIGGCI	GIGCIICIGI	CTCATCTTT	ATCACACACC
12/851	TTCTGGGGTT	CAGAGCAATT	GIGCICIGCC	CICATCITI	ATGACACACC
127901	TAGCAAAACA	GAAGCAGAGG	AGCGAGTTGA	AACAGACAAA	CGACTATCIG
127951	TTATTCTTCA	<b>AACATGCCTA</b>	GGATTGTATT	TAACTATCAC	CTATCTAAAA
128001	GAGGTATTCT	CGCCTGCCTG	GAAAGAATTT	TGCTAAGAAA	ATTGTTTCTC
128051	TTCTTCCCAT	ΔΤΤΔΤΤΤΤΔ	CTCTATGCTA	GTTCCCTGTG	ATTTGATATG
120031	TCAACTTTGA	CAAATTCATT	TTTCTAAAGC	ACAGATATGA	CCTTTTTTGT
120101	TCAACTITGA	CAAATICATI	TOTTOTALAGE	TCCTACACAC	ACACACACAC
158121	TAAGAAAAAG	AAACIACIGI	IGCICCCAG	TGCTACACAC	ACACACACAC
128201	ACACATACAC	ATACACACCC	TTCACAAGCC	TIAICIGCAC	CCCCGCCCAC
128251	TCCCCACAAC	AAACTTCAGA	TGTCTTAGCT	TGGCATTCTT	CGGAATTAGG
128301	TCAACGTTTC	<b>AGATTTTGCT</b>	TCCATTTGTG	TATTTCTGAC	CCTTCATGAA
128351	CTCATTTTGG	CCTCTTAGAA	CTTCTTCCTC	TTCTCAAAGC	ATCTCTTGGG
128401	TTTTTTAACC	TCTTGTTCCT	TCGCCTATAA	AGAGAGTTTC	CAAGGCAAAC
120401	CTTGGTCTTC	TTTAAAAATC	ACTCTCCCTA	AGATTTGAAA	TCACTAAATG
120431	CITGGICITE	AAACCATATA	TCTTCATTCC	ACCCCTTTTC	AAAATCTTTA
178201	AAGTTTTAAT	AAAGGATATA	TCTTCATTGC	AGGGCTTTC	TTAAACTATT
128551	TAGCCAAGTA	TTTTGGTCAT	TICTAAGAAA	GGACACACTA	TIAAACTATI
128601	CCAGTTCGTG	TTGGGGAGGT	TTTTCTAGAT	CTCTTTATAT	TCAAATTCTA
128651	TTCATACTTT	ATCACCTATG	ACAAAATAGC	ACTITCTCTA	AAGAAACATT
128701	CTCTGACCTC	CCTATCTAAA	GTGATCCGAA	TCTCTTCCAA	ACATTTATTT
128751	<b>ACTTTATGTA</b>	TCCTGTGAAT	CTTTGGAATC	TAAGCTTATT	AGAAAATATA
128801	GAAAACCACG	AAAATGAAAG	CAAAAATCAG	CTGTAGTCTC	TAAGGCAAAG
128851	AACATTTCCA	ΑΤΤΑΑΘΑΑΑΤ	TAAACTCCCT	TTGACTTTTA	AACCCCATCT
120031	TAGCAGTTTG	TTCCATTCAC	TTCCAACTTC	TTTCTCTTCT	CATAAGGATA
120901	CTCTATCTTC	ACATACATAC	ATATACATAC	ATCTCTTCTT	TTACCAAAAA
178821	CTCTATCTTC	AGATAGATAG	ATATAGATAG	AIGIGIIGII	TTTCATAGCA
129001	TAGAAGTATG	TTTTACCTTG	TTGAGCCTTI	HHIIIICA	TTTCATAAGA
129051	TAAAATGTAC	AGCTTTCTAG	ATCAGAACAC	CTAAATCTAT	TTICITITA
129101	AGGATTAAAT	CTATAGGCAT	ATCAATTTTT	ATTTTTTATC	TCTTGTATAT
129151	TATTAGGTTG	TTAATTCATT	AAAGGTAAAG	TATGTATCTT	ATATAGGTTA
129201	GTATTATTCA	CAGTATTTAA	CTGTTTTTT	TTTCCTCAGG	AGAGTCTTGC
120251	TCTGTCCCCC	AGGCTGGAGT	GCAATGGCCC	AATCTCGGCT	CACTGCAACC
120201	ACCCCCTCCT	CTCTCCAATC	AACCCTCCCG	CCTGAGCCTC	CCAAGTAGCT
12001	GGGACTACAG	CONTATCCCA	CCATCCCTCC	AAATTTTTG	TATTTTTCT
173331	. GGGACTACAG	TOTTACCATO	TTCCCCACCC	TACTCTTCAA	CTCCTCCCCT
129401	. AGAGIIGGGG	ICTIACCATG	TIGCCCAGGC	CTCCTCCCAT	CTCCTGGGCT
129451	. CAAGCAATCC	ACCTGCCTTG	GCCCTGCAAA	GIGGIGGGAI	TACAGGTGTG
129501	. AGCCGCCGCA	CCTGGTCACA	. ATATTTAACT	TTAAATAGGT	ATATAATACA
129551	. TGGTTATTTT	CACTCACATO	: CATGTGAAGA	GACCACCAAA	CAGGCTTTGT
129601	GTGAGCAACA	AGGCTATTTC	ACCTGGGTTT	CAGGTGGGCT	GAGTCCGAAA
129651	AGAGAATCAG	CGAAGGGAGA	TAGGAGTGGG	GCCGTTTTAT	AAGATTTGGG
120701	TAGGTAAAGG	AAAAAGGGGG	GTTGTTCTCT	GGTGGGCAGG	GGTGAGGATC
120751	ACAACCTCCT		CGTTTTGAGG	CAGGATGAGG	CAGGAGAAGG
120001	ACAAGGIGCI	CCTACTCTC	TCACTTAACC		CCATTITCAC
T53801	LAATITCACAA	GGIAGIGICA	1 CAGTTAAGG	CAUGAACCUG	CCATTTTCAC
T5882]	LITCITTIGTG	GIGGAATATC	. AICAGITAAC	GCAGGAACCA	GCCATCTGGA
129901	L TGTGTATGTG	CAGGTCACAG	GGGATATGAT	GGCTTAGCTT	GGGCTCAGAG
129951	L GCCTGACAGT	TATTGAATGA	<b>ATGGAGAAA</b> C	: AAATCACTTA	GACACCTTCT
130001	L AGGAAAAAT	GACCAACTAT	GCTACCTGCA	\ ATTACGTTTC	AAAATGTAGC
130051	ΤΤΑΤΟΤΘΔΑΘ	AAAAGGAAGT	AACATTTAAT	TACAAGCATC	AATACAACTC
130101	A A G C A C A G A C	GAAGTGTGCT	ΔΔΔCΔΔΤΤΤ	CTCCATACGT	ACAAATTTTT
130101	L ATTTACAGAA	AAGTATATG	CTTAATGAGA	AAATGTGCTC	GAAAACATTC
TOOTO	LATTIACAGAA	AAGIAIAIGI	CITATIONO	· AMIDIACIO	

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130201 TCATCATTTC TGAGTTTGGT TTCAGTCTTA ATGAATGTGT CO	CLIAACIA
1202E1 TEAATCTCCT TTGTCATCTC TCTAACICCC IACIAICICA I	GCCALIGC
120201 AAACCCAAAC CTCCACATCT TITATAGIII CATAITAICC P	AMMOIDIIA
120251 ACTTACCATA CATGTGTACA TAGTTTTGTA CICALIGIAC A	IGCLINGCI
120401 CCAATTCTTT TCCCTTTGCA CTTCTGAAAL ACAACCATAL !	
130401 GCACTITOTTIC CCTTATAACA TITCACCTTT TCCACTITGT T	TATTCTCTA
130451 TCATTIGITE CETTATAGA TITCACCTT ACCEPTATA	ΔΤΔΤΔΤΑ
130501 TATGCTCACT GTTAGTTTAG ATGCTGCCTT AGGCTTTTAT G	TTATTTAA
-120FF1	111711177
120601 CTCTCTCTCT CTCTGTGTAT ACAGTCIAIA IAAIAAAIII A	CAIGCLICC
120CE1 TTAACTACAC TCTACCCCCC ACCAACALAG AAACCALAIG I	GICIIGIIC
120701 TTCATTCTAC CCTCAATGCC TAAGAAAGGI GCIGGAACAI G	GIAGGCAII
130751 CAATAAATAA TTGGTAAATA AATAAATATA CAATTCTGGT A	GTTGATTAA
130801 TTCAAATTAA TTTTAAAATT TAGAACTGTA AAAGTAAATT A	AAAAATAAG
130801 II CAAATTAA TITTAAAATT TAGAACTAA CCAACAGGTC A	TGGAGATTT
130851 ATAAAGACAA TGTGATTATT TTTTAATAAA CCAACAGGTC A	AGAAAAATG
130901 TAAAAATTAA ATTCAGTCAT ATGGCCTTGT AAAGTAACTA G	TCATTTCTT
130951 TACACACTTA AACCAGCTGC TTGTGGCATT CATCAGTTAA T	CTTCACAAC
121001 TATAAATCA TIITATIITO TAGGIGGGG CO AGAAACAGIA V	OFFICIALITY
- 1210Ε1 - ΚΑΚΚΑΤΚΑΑ ΤΤΑΚΑΚΤΟΔΑ ΘΔΔΘΔΔΑΘΑΘΑΘΑΘΑΚΑΚΑΘΙ Μ	AAAACACAT
- 121101 CTCCATACAC ATATAAGCCT AGAAGCIIGA GIAIACIAAG C	CIAKICIOA
131151 TTCTTAATGA TAAACATGGT CTGAATCATA TGGAGTAACC T	AACCCTTTG
131201 GCTACTAAAT TACCAATAAA CATTGATAAT GGTGATAAAG C	ATCTAGCAC
131201 GCIACIAAA IACAAIAAA CATTAAT TICTACTATA T	ΔΑΤΤΑССΑΑ
131251 TCCTTTACTG ATATTGAGTT AATGAGTTAT TTCTACTATA T	CCTAAATAT
131301 GACATATGAT ATAGCTATGG TCCTTTATTT AGTGTTGAGG	CAATTAATC
131351 GGCAGTTGTT TITAGATCTT ACTTAAAAAG CAAAAATGTT 1	CAATICATCA
121401 TCCCTTTCAA GGGCCACCTC CTGGCACTIC AIGGIICCAI S	JAATAGCTGA
$-$ 121 $A$ E1 $C$ ATTCACTTC $C$ CATCTCT $\Delta$ A $\Delta$ ATTAA $G$ C $G$ C $G$ CLCCAL $G$	ACHILLI
121E01 CACCACTCAT TTTGCTGTTC ACTATTCALL CACALLIACA	AIGCCCALL
121EE1 TTTACCTTTC TCTCAATAAT GATAAAAAIC ICICICIAI A	ALIGIGICIA
131601 ATACTATTAG CCACTCACTC TGTTGAGAAA TTTACACATA	TATCTCCTT
131651 TAATITITCC AGCAATCTCA TGAGGTAGCT CATTITACAG	TGAAGTAAC
131651 TAATTTICC AGCAATCTCA TGAGGTAGCT CATTTACC	ΓΤΤΔΑССΤСΑ
131701 AAGCTCAGAA ATTGAGTGGA GAAGTTTAGC ACCAAATCCT	TACAGGGAA
131751 AACACATGAT TATTITATAT TACCTCTTAA CACTGATTTA	
121001 AAACTTAAAC CCTTTCATTT CCCCCAAIII AGGICAICCA	CAACAGICA
1210E1 TTATTAAAT ATCTTAAAAG GGCCAGGCAL GIGALCAAIG	IGIAIAICCA
121001 TATTAACTET GETETEGETA GTTAATEGAA TATGGAAATT	HUHCAHA
1210E1 AATAAACATC TATTGTGCAC CIACIGAAIG CIIGGICICA	
122001 TOATATAATO TOTGGOTGTG AGTATOTIAL AGIILALAIA	AGAGACATGA
132051 AATTTCAGTG TTGGTGAGTC CCCTACAAAA TAATATAGAT	AAAGGCTGTC
132101 CTCTAGTGTA AAGCTGTGAA AACTACAGCT AATCCACAGT	TTTCTTTTGT
132101 CTCTAGTGTA AAGCTGTGAA AACTACAGCT AATCCAGCT	ΔΔΔCTGTAGA
132151 TTAATTICTT TTCTTTTAA ATTACTTTTC TTCAAAATTA	TECCTCATCA
132201 AGAACCTGGT TCTTCCCCCA AAATTTTTTT TAAAAGCTTC	TCATAGCATT
132251 CAAAATTCTC CACCCTGCCA TACTCTGTGG AACCAGGGAC	CTCACCTTCC
122201 TOTOCOACTO CAGTTGATGT TTTCTGAGCA GILLICIGIC	(   [::Δ[::[     [:].].
122251 TCATTATCTT CCAGTGAAG GGATGGIAIG GIAAAAIICI	COATTACTT
	GGATTIACTI
122401 CCAATCAACC CTTACATAAT AATTITIIAG ACIICCAIII	ATTGAGGACT
132401 GCAATCAACC CTTACATAAT AATTITITAG ACTICCATTI	ATTGAGGACT AAACAATTTC
132401 GCAATCAACC CTTACATAAT AATTITITAG ACTICCATTI	ATTGAGGACT AAACAATTTC
132401 GCAATCAACC CTTACATAAT AATTITITAG ACTICCATTI 132451 TGTCCAGTAT TTCGTGTTAA TACTTATATA ATACCTTATA 132501 AAATCAGCAT CTCAGAGGCT GATTCAGTCC ACTTGAATGT	ATTGAGGACT AAACAATTTC TTTGTTTGGC
132401 GCAATCAACC CTTACATAAT AATTITITAG ACTICCATTI 132451 TGTCCAGTAT TTCGTGTTAA TACTTATATA ATACCTTATA 132501 AAATCAGCAT CTCAGAGGCT GATTCAGTCC ACTTGAATGT	ATTGAGGACT AAACAATTTC TTTGTTTGGC AGCGACCATA
132401 GCAATCAACC CTTACATAAT AATTITITAG ACTICCATTI 132451 TGTCCAGTAT TTCGTGTTAA TACTTATATA ATACCTTATA 132501 AAATCAGCAT CTCAGAGGCT GATTCAGTCC ACTTGAATGT 132551 TCAGTGGAGT GTTCAACTTT AAAATTTATG GTATTTTAGA	ATTGAGGACT AAACAATTTC TTTGTTTGGC AGCGACCATA AACACAGGAC
132401 GCAATCAACC CTTACATAAT AATTITITAG ACTICCATTI 132451 TGTCCAGTAT TTCGTGTTAA TACTTATATA ATACCTTATA 132501 AAATCAGCAT CTCAGAGGCT GATTCAGTCC ACTTGAATGT 132551 TCAGTGGAGT GTTCAACTTT AAAATTTATG GTATTTTAGA 132601 AATTCCTAGT GTCTCTTTAA GAAAAAGTAG GGGGTCTGGC	ATTGAGGACT AAACAATTTC TTTGTTTGGC AGCGACCATA AACACAGGAC TTAGAAATTG
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132401 GCAATCAACC CTTACATAAT AATTITITAG ACTICCATTI 132451 TGTCCAGTAT TTCGTGTTAA TACTTATATA ATACCTTATA 132501 AAATCAGCAT CTCAGAGGCT GATTCAGTCC ACTTGAATGT 132551 TCAGTGGAGT GTTCAACTTT AAAATTTATG GTATTTTAGA 132601 AATTCCTAGT GTCTCTTTAA GAAAAAGTAG GGGGTCTGGC 132651 CACCTACACA TATGGCAACG CAAGAGTCAG CTGGACAGGG 132701 ATATAGATAT TTTATCGGTT GAAAGTTTAG CTTGGAAACA	ATTGAGGACT AAACAATTTC AGCGACCATA AACACAGGAC TTAGAAATTG TTTGGAAATTG TTTGGAAATTC CTTTTCTCCC
132401 GCAATCAACC CTTACATAAT AATTITIAG ACTICCATTI 132451 TGTCCAGTAT TTCGTGTTAA TACTTATATA ATACCTTATA 132501 AAATCAGCAT CTCAGAGGCT GATTCAGTCC ACTTGAATGT 132551 TCAGTGGAGT GTTCAACTTT AAAATTTATG GTATTTTAGA 132601 AATTCCTAGT GTCTCTTTAA GAAAAAGTAG GGGGTCTGGC 132651 CACCTACACA TATGGCAACG CAAGAGTCAG CTGGAAACA 132751 TTTTTTTTCT TTTGTCCTAT ACAAATGAAG ACTTTTACTT	ATTGAGGACT AAACAATTTC TTTGTTTGGC AGCGACCATA AACACAGGAC TTAGAAATTG TTTGGAAATTG CTTTTCTCCC GGAAATTGTA
132401 GCAATCAACC CTTACATAAT AATTITIAG ACTICCATTI 132451 TGTCCAGTAT TTCGTGTTAA TACTTATAA ATACCTTATA 132501 AAATCAGCAT CTCAGAGGCT GATTCAGTCC ACTTGAATGT 132551 TCAGTGGAGT GTTCAACTTT AAAATTTATG GTATTTTAGA 132601 AATTCCTAGT GTCTCTTTAA GAAAAAGTAG GGGGTCTGGC 132651 CACCTACACA TATGGCAACG CAAGAGTCAG CTTGGAAACA 132751 TTTTTTTTCT TTTGTCCTAT ACAAATGAAG ACTTTTACTT 132801 TTAAGAGACC GTATCATATTT CGCTCCAGTA CTTCCAGCAA	ATTGAGGACT AAACAATTTC TTTGTTTGGC AGCGACCATA AACACAGGAC TTAGAAATTG TTTGGAAATTG CTTTTCTCCC GGAAATTGTAGGAAATTG
132401 GCAATCAACC CTTACATAAT AATTTITIAG ACTICCATTI 132451 TGTCCAGTAT TTCGTGTTAA TACTTATAA ATACCTTATA 132501 AAATCAGCAT CTCAGAGGCT GATTCAGTCC ACTTGAATGT 132551 TCAGTGGAGT GTTCAACTTT AAAATTTATG GTATTTTAGA 132601 AATTCCTAGT GTCTCTTTAA GAAAAAGTAG GGGGTCTGGC 132651 CACCTACACA TATGGCAACG CAAGAGTCAG CTGGACAGGG 132701 ATATAGATAT TTTATCGGTT GAAAGTTTAG CTTGGAAACA 132751 TTTTTTTTCT TTTGTCCTAT ACAAATGAAG ACTTTTACTT 132801 TTAAGAGACC GTATCATATATT CGCTCCAGTA CTTCCAGCAA 132801 CACACGTTTG AGACGACTGT TGTAACTTAC CCTTCTGCCT	ATTGAGGACT AAACAATTC TTTGTTTGGC AGCGACCATA AACACAGGAC TTAGAAATTG TTTGGAAATT CTTTTCTCCC GGAAATTGTTTCTCCC GGAAATTGTA GGTCACAGGA TGTCCAAACG
132401 GCAATCAACC CTTACATAAT AATTTITIAG ACTICCATTI 132451 TGTCCAGTAT TTCGTGTTAA TACTTATAA ATACCTTATA 132501 AAATCAGCAT CTCAGAGGCT GATTCAGTCC ACTTGAATGT 132551 TCAGTGGAGT GTTCAACTTT AAAATTTATG GTATTTTAGA 132601 AATTCCTAGT GTCTCTTTAA GAAAAAGTAG GGGGTCTGGC 132651 CACCTACACA TATGGCAACG CAAGAGTCAG CTGGAACAG 132701 ATATAGATAT TTTATCGGTT GAAAGTTTAG CTTGGAAACA 132751 TTTTTTTTCT TTTGTCCTAT ACAAATGAAG ACTTTTACTT 132801 TTAAGAGACC GTATCATATT CGCTCCAGTA CTTCCAGCAA 132851 CACACGTTTG AGACGACGG CTCTCTGGCT TAAGTTTAGA	ATTGAGGACT AAACAATTTC TTTGTTTGGC AGCGACCATA AACACAGGAC TTAGAAATTG TTTGGAAATTG TTTTGGAAATT CTTTTCTCCC GGAAATTGTA GGTCACAGGA TGTCCAAACG AGTTAGTATA
132401 GCAATCAACC CTTACATAAT AATTTITIAG ACTICCATTI 132451 TGTCCAGTAT TTCGTGTTAA TACTTATAA ATACCTTATA 132501 AAATCAGCAT CTCAGAGGCT GATTCAGTCC ACTTGAATGT 132551 TCAGTGGAGT GTTCAACTTT AAAATTTATG GTATTTTAGA 132601 AATTCCTAGT GTCTCTTTAA GAAAAAGTAG GGGGTCTGGC 132651 CACCTACACA TATGGCAACG CAAGAGTCAG CTGGAACAG 132701 ATATAGATAT TTTATCGGTT GAAAGTTTAG CTTGGAAACA 132751 TTTTTTTTCT TTTGTCCTAT ACAAATGAAG ACTTTTACTT 132801 TTAAGAGACC GTATCATATT CGCTCCAGTA CTTCCAGCAA 132851 CACACGTTTG AGACGACGG CTCTCTGGCT TAAGTTTAGA	ATTGAGGACT AAACAATTTC TTTGTTTGGC AGCGACCATA AACACAGGAC TTAGAAATTG TTTGGAAATTG TTTTGGAAATT CTTTTCTCCC GGAAATTGTA GGTCACAGGA TGTCCAAACG AGTTAGTATA
132401 GCAATCAACC CTTACATAAT AATTTITIAG ACTICCATTI 132451 TGTCCAGTAT TTCGTGTTAA TACTTATATA ATACCTTATA 132501 AAATCAGCAT CTCAGAGGCT GATTCAGTCC ACTTGAATGT 132551 TCAGTGGAGT GTTCAACTTT AAAATTTATG GTATTTTAGA 132601 AATTCCTAGT GTCTCTTTAA GAAAAAGTAG GGGGTCTGGC 132651 CACCTACACA TATGGCAACG CAAGAGTCAG CTGGAACAGG 132701 ATATAGATAT TTTATCGGTT GAAAGTTTAG CTTGGAAACA 132751 TTTTTTTTCT TTTGTCCTAT ACAAATGAAG ACTTTTACTT 132801 TTAAGAGACC GTATCATATT CGCTCCAGTA CTTCCAGCAA 132851 CACACGTTTG AGACGACTGT TGTAACTTAC CCTTCTGCCT 132901 AATGTGTGCA CTTCTTAAAA AGGTAAGAAG GAAGACTGCA 132901 CAATATTGGG GACAGTCATG ATAGTATACA TTTGTAGAGT	ATTGAGGACT AAACAATTTC TTTGTTTGGC AGCACCATA AACACAGGAC TTAGAAATTG TTTGGAAATTG CTTTTCTCCC GGAAATTGTA GGTCACAGGA TGTCCAAACG AGTTAGTATA GTATTTTCTA
132401 GCAATCAACC CTTACATAAT AATTITIAG ACTICCATTI 132451 TGTCCAGTAT TTCGTGTTAA TACTTATAA ATACCTTATA 132501 AAATCAGCAT CTCAGAGGCT GATTCAGTCC ACTTGAATGT 132551 TCAGTGGAGT GTTCAACTTT AAAATTTATG GTATTITAGA 132601 AATTCCTAGT GTCTCTTTAA GAAAAAGTAG GGGGTCTGGC 132651 CACCTACACA TATGGCAACG CAAGAGTCAG CTGGACAGGG 132701 ATATAGATAT TTTATCGGTT GAAAGTTTAG CTTGGAAACA 132751 TTTTTTTTCT TTTGTCCTAT ACAAATGAAG ACTTTTACTT 132801 TTAAGAGACC GTATCATATT CGCTCCAGTA CTTCCAGCAA 132851 CACACGTTTG AGACGACTGT TGTAACTTAC CCTTCTGCCT 132901 AATGTAACAA AGGAAGCAGG CTCCTCTGGCT TAAGTTTAGA 133001 CAATATTGGG GACAGTCATG ATAGTATACA TTTGTAGAGT	ATTGAGGACT AAACAATTTC TTTGTTTGGC AGCGACCATA AACACAGGAC TTAGAAATTG TTTGGAAATTG TTTTGCCC GGAAATTGTA GGTCACAGGA TGTCCAAACG AGTTAGTATA GTATTTCTCA AGATTCCCCT
132401 GCAATCAACC CTTACATAAT AATTITIAG ACTICCATTI 132451 TGTCCAGTAT TTCGTGTTAA TACTTATAA ATACCTTATA 132501 AAATCAGCAT CTCAGAGGCT GATTCAGTCC ACTTGAATGT 132551 TCAGTGGAGT GTTCAACTTT AAAATTTATG GTATTITAGA 132601 AATTCCTAGT GTCTCTTTAA GAAAAAGTAG GGGGTCTGGC 132651 CACCTACACA TATGGCAACG CAAGAGTCAG CTGGACAGGG 132701 ATATAGATAT TTTATCGGTT GAAAGTTTAG CTTGGAAACA 132751 TTTTTTTTCT TTTGTCCTAT ACAAATGAAG ACTTTTACCT 132801 TTAAGAGACC GTATCATATT CGCTCCAGTA CTTCCAGCAA 132851 CACACGTTTG AGACGACTGT TGTAACTTAC CCTTCTGCCT 132901 AATGGTGTCA CTTCTTAAAA AGGTAAGAAG GAAGACTGCA 133001 CAATATTGGG GACAGTCATG ATAGTATACA TTTGTAGAGT 133051 GCTGTTAGCT TTCAAATACA TGGCTTCATT AACTCAACTC	ATTGAGGACT AAACAATTTC TTTGTTTGGC AGCGACCATA AACACAGGAC TTAGAAATTG TTTGGAAATTG TTTTCTCCC GGAAATTGTA GGTCACAGGA TGTCCAAACG AGTTAGTATA GTATTTTCTA AGATTCCCCT ATGCTTTGTC
132401 GCAATCAACC CTTACATAAT AATTITIAG ACTICCATTI 132451 TGTCCAGTAT TTCGTGTTAA TACTTATAA ATACCTTATA 132501 AAATCAGCAT CTCAGAGGCT GATTCAGTCC ACTTGAATGT 132551 TCAGTGGAGT GTTCAACTTT AAAATTTATG GTATTITAGA 132601 AATTCCTAGT GTCTCTTTAA GAAAAAGTAG GGGGTCTGGC 132651 CACCTACACA TATGGCAACG CAAGAGTCAG CTGGACAGGG 132701 ATATAGATAT TTTATCGGTT GAAAGTTTAG CTTGGAAACA 132751 TTTTTTTTCT TTTGTCCTAT ACAAATGAAG ACTTTTACTT 132801 TTAAGAGACC GTATCATATT CGCTCCAGTAA 132851 CACACGTTTG AGACGACTGT TGTAACTTAC CCTTCCAGCAA 132901 AATGGTGTCA CTTCTTAAAA AGGTAAGAAG GAAGACTGCA 133001 CAATATTGGG GACAGTCATG ATAGTATACA TTTGTAGAGT 133051 GCTGTTAGCT TTCAAATACA TGGCTTCATT AACTCAACTC	ATTGAGGACT AAACAATTTC TTTGTTTGGC AGCGACCATA AACACAGGAC TTAGAAATT CTTTTCTCCC GGAAATTGTA GGTCACAGGA TGTCCAAACG AGTTAGTATA GTATTTCTCA AGATTCCCT ATGCTTTGTC GCTTCTCTAT
132401 GCAATCAACC CTTACATAAT AATTTITIAG ACTICCATTI 132451 TGTCCAGTAT TTCGTGTTAA TACTTATATA ATACCTTATA 132501 AAATCAGCAT CTCAGAGGCT GATTCAGTCC ACTTGAATGT 132551 TCAGTGGAGT GTTCAACTTT AAAATTTATG GTATTITAGA 132601 AATTCCTAGT GTCTCTTTAA GAAAAAGTAG GGGGTCTGGC 132651 CACCTACACA TATGGCAACG CAAGAGTCAG CTGGACAGGG 132701 ATATAGATAT TTTATCGGTT GAAAGTTTAG CTTGGAAACA 132751 TTTTTTTTCT TTTGTCCTAT ACAAATGAAG ACTTTTACTI 132801 TTAAGAGACC GTATCATATT CGCTCCAGTA CTTCCAGCAA 132851 CACACGTTTG AGACGACTGT TGTAACTTAC CCTTCTGCCT 132901 AATGGTGTCA CTTCTTAAAA AGGTAAGAAG GAAGACTGCA 133051 GCTGTTAGCT TTCAAATACA TGGCTTCATT AACTCAACTC	ATTGAGGACT AAACAATTTC TTTGTTTGGC AGCGACCATA AACACAGGAC TTAGAAATTC TTTGTTTCCC GGAAATTGTA GGTCACAGGA TGTCCAAACG AGTTAGTATA GTATTTCTCA AGATTCCCT ATGCTTTGTC GCTTCTCTAT GTCATACTGC
132401 GCAATCAACC CTTACATAAT AATTITIAG ACTICCATTI 132451 TGTCCAGTAT TTCGTGTTAA TACTTATAA ATACCTTATA 132501 AAATCAGCAT CTCAGAGGCT GATTCAGTCC ACTTGAATGT 132551 TCAGTGGAGT GTTCAACTTT AAAATTTATG GTATTITAGA 132601 AATTCCTAGT GTCTCTTTAA GAAAAAGTAG GGGGTCTGGC 132651 CACCTACACA TATGGCAACG CAAGAGTCAG CTGGACAGGG 132701 ATATAGATAT TTTATCGGTT GAAAGTTTAG CTTGGAAACA 132751 TTTTTTTTCT TTTGTCCTAT ACAAATGAAG ACTTTTACCT 132801 TTAAGAGACC GTATCATATT CGCTCCAGTA CTTCCAGCAA 132851 CACACGTTTG AGACGACTGT TGTAACTTAC CCTTCTGCCT 132901 AATGGTGTCA CTTCTTAAAA AGGTAAGAAG GAAGACTGCA 133001 CAATATTGGG GACAGTCATG ATAGTATACA TTTGTAGAGT 133051 GCTGTTAGCT TTCAAATACA TGGCTTCATT AACTCAACTC	ATTGAGGACT AAACAATTTC TTTGTTTGGC AGCGACCATA AACACAGGAC TTAGAAATTC TTTGTTTCCC GGAAATTGTA GGTCACAGGA TGTCCAAACG AGTTAGTATA GTATTTCTCA AGATTCCCT ATGCTTTGTC GCTTCTCTAT GTCATACTGC

133301 NNNNNNNNN NNNNN	NNNNN NNNNNNNNN	NNNNNNNN	ИМИМИМИМ
133351 NNNNNNNNN NNNNN	NNNNN NNNNNNNNN	MMMMMMMM	Alalalalalararara
133401 NNNNNNNNN NNNNN	NNNNN NNNNNCTAGC		GTTTGTCCAC
122451 ATACACTITT ACCAC	TCCAT TCTATTCCCC	ATGCAGCCCC	ACAGIGGICI
133501 GTTAAAGGAC AGTCC	AGGAT ATTTTCCIIA		AAAGATTAAA
133551 ATAATTTTGT GGTAC	ΛΔΔΔG ΤΙΚΔΔΔΔΙΑΚ	CICICAAGCC	TTGTTTTGGA
433CO1 CTTTCTCCACT TTTCT	CCCCC CTTTGACTAC	ACATAAACTG	CTTIGGCCTT
122CE1 TTTCTTCTTC TITTC	דדדכד דדדכדככדדכ	TTCACTTTIA	CATACCAGIC
122701 TTCCTCTCAC CACAG	GACCT TTGCACATGC	CAGIACCIAI	I CC I GGAACA
122751 CTCCCTCCAA TCCTA	CTTCC TCCAGTTCC	( CIIIGAGAGC	AGIACIACIC
433001 AATCTCCTTC ACTGG	TTCTA GILLAIGAAI		GOICIAIIO!
4330E4 AACTAAACAA CTTCA	.C. A C. A A A A A A A A A A A A A A A A	LACILIAIAG	
122001 CTCCTCTACC ATCTA	ΛΛΓΔΓ ΔΙGΔΙΚΑΑΙΚ	GACITATO	A I I UAAAUAO
433051 CTCCAACCTT CTTTC	: ACCCCT 11-111-AAC 10	AAGILACAAG	GIGICIAIGI
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4340E1 CCATTCCAAA TTCAA		ALAAAAA IAA	CIUMCCCIIC
134101 TACATAGTTT GGGAA	AGCACA ACTITAGCTO	TIAGCICAAA	TITITCACCITC
1241E1 TTCCTCTAAG TTCA(	ΈΔΤΔΔΟ ΑΚΙΑΙΚΙΙΙΚ	_ CITCATAGCA	1111100011
134201 TAAAATTATA CCCAC	CATTT GTGTGATCC	CACATCTCTT	ACCATTGTAT
134251 CTTAGCTTCA TGAGG	GGTAGG GACCATGIC	T CAAATTTGAC	AAGTATTCAA
134301 TCTCAGCATC TAACA	ACAAAG CCIGAGAAG	T TTCAAGGTAC	CCATCTTCAT
134351 ATAAATGAGG TCCAG	CAGCTT TCATCAGAT		TATATTGAGT
134401 CAAACAGATG AAGA	ACAGII AIAGCGGGA	A CACCAATGGG	
134451 GATGATACAA AACA	AGAATG AGGGGCCCA	C CACAAAATTG	CACCAGTTGT
134501 TITTTTTTT TTTT 134551 GGCTGGTAAT GGAA	AATACC TITACTCCC	T AAGGAGTCAT	CATTTGTGTC
134551 GGCTGGTAAT GGAA 134601 TCTTGTTTTT GGAG	TO A CT TO CTT ATT	T GGAATAGGGA	CATTGCATCA
134601 TCTTGTTTTT GGAG 134651 GTAATGTCAA AGAC	ATACAA TCCCCCATC	A TITTICATAA	GCAAATTCTG
134651 GTAATGTCAA AGAC 134701 CTTAGTTCCA AGAC	ACCCCT CCTTCACTC	C ACAAATTACA	CCCTGAGGTT
134701 CTTAGTTCCA AGAC 134751 GCATGGTTGT CATC	TTCACA ACCATTCTC	A AGTGGGACTG	ACAATGCCTA
134/51 GCATGGTTGT CATC	TTOCTO TOATGTTGG	C TCAGGAATGG	TTAAGGGGGC
134851 AAAAATCTTT TATC	TCAATT AGTAAAATC	T AGAACTATAA	CAGTTACTTT
134901 AGTTACACCT TATC	TATECC GCCCCAAT	G TATTTTAATT	AGTTGTAAAA
1240E1 ACACCTACAA TTCT	TAGTAG GAAAIGAGI	T CTACTTGTGA	AATGTATCAA
135001 CATTTGTCAC CATA	GGTTTT CTACIAGGI	A CHIGIAIAA	MINGCCICCC
135051 ACTAATCCTG ATTA	CAATCG TATGAAATA	C ALIALIACCA	CITITION
135101 ACACATGGGT AAAC		IN NNNNNNNNN	NNNNNNNNN
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135651 CCGGTGTGCC AGA 135701 GTTAAGAGAG CCC	CAATTCC CATTTAC	CA AACCTACCA	A GTAGTCAAGC
135701 GTTAAGAGAG CCC 135751 CACAGGGTAA GTT	IGICACC AAAGGICA	CT GAAGTTCTA	CTTTTAACCA
135751 CACAGGGTAA GTT 135801 TGGGATTCTA ATC 135851 CTTTTTATGG TCT	CAGGIGI ATTIGCGA	AN GTCCTAGTT	CCCAAATAGT
135851 CTTTTTAIGG ICT	CTCCTCC CCTTTTT	TT AAGTTITCT	TGATTCTAAA
135901 CATTCTCATG AAT 135951 GATGCAGAAG TTT	CTCTCCC TAGAGATC	TG AGTCAAAGA	A TTGAAAATTG
135951 GATGCAGAAG III 136001 TTGGAGTTGG GGT	CACCAAT TTATTTTA	GC ATTTGCCCC	T CATCCTTTGT
12CAE1 TTCTTCTC TCA	CCCATTT ALAILIGI	AA GUACIUAIA	4 6666666
12C1O1 ATAATTCCCA TTC	CATCGAT AGCCAAAL	CA AIGGACIIC	I GIGGICIACI
43C1E1 CCATTATCCT CCT	***************************************	GA AGULLIAGGU	
43C3O1 4CTC4CCCCA CTA	CCTCCTT ( ) ( ) ( ) ( )	L I AMAGE I UAA	A 1171719119
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136351 TCAGCACTTT AGG	AGGCCGA GGCAGGAG	GA TCAGGGGTT	C AAGATCAGCC
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136401	TTGGCAACAT	GGCAAGACCG	TGTCTCTACA	GAAAAGAAA	AAAAAATTAG
126/51	CCACCCCTCC	TGGTACTTGG	GTGTAGTCIC	AGCTACCTAG	GAGGC I GAGG
126501	TAGAAAGATC	ΔϹͳΤΔΔGCCC	AGGAGTIIGA	GGCTGCATGA	GCAGIGATIG
126551	TGCCACTGCA	CTCTAGCCTG	GGTAACAGAG	IGAGACCCIG	ICICAAAAAA
126601	ΛΛΛΛΛΛΔΔΤ	TACTCTTAAG	CCCATATGAG	GCALLIGCIG	IGGGAAIGIG
126651	ACACTCTCAT	CCTTCATGTA	CACACAGCAG	GAGGCATGCT	CCAATGAGAG
126701	CCTAACGAGA	ΛΛΩΤΛΟΛΛΑΘ	TGAGAGAAAG	GAGAAAGCAG	GGIGGIGGAA
126751	TTCTACCTTA	TGGAGCAACA	GGAGGGTAGG	ICIGAGIICI	TACCICICG
126001	CTTTCTCCCC	TCCATTAGGG	GCAACTIGIA	CCATAATIGA	CACATGACAC
126051	A ATC A ACCTC	TAGGCACCC	AACTCTTGCI	ICCCCCICCI	ICIAIGIGII
126001	CCCTCCTCC	ΔΔΤΤΔGCCΔΤ	CAATGCTGGC	ICAAAAGAAG	FICIACGITA
126051	TECTTCTCTG	<b>ACTITAGTGT</b>	GAATCGGAAT	CATCIGGGAA	GCICATIAAA
127001	CTCCAAGTTC	TTGGACCTCA	CATTCTGAAA	HCIGATIIG	GGAAGICIGG
127051	TTGGAGAACT	GGGAAGCTGA	GCAAGCAACT	IAGGIGATIC	IGAGITACAT
127101	CATTATTAGA	GCGCACTTTC	GGAAACATAA	CCCAAAAIII	ATTICCACT
127151	TTACAAAAAT	<b>AACTGTAAGT</b>	CGGCTTTTGT	ITTIACICAT	IGAGGCCTAA
127201	TTGAGAGTTT	ΔGΔΔΔΔΤΔΔ	ACGAAGAATA	IGAAAAACGA	IGCIGGCAAI
127751	$\Lambda \Lambda \Lambda T \Lambda \Lambda C C T \Lambda$	ΔΔΔΥΤΤΔGΔG	TGGGAATCCC	AGIGIATIAI	TCATGGACTG
127201	CTCCGTTAAG	<b>ACTAAGTATT</b>	ATTTTCCGTA	ITAGGICIGC	IGIGITITIC
127251	ACAATGATAC	ΔGTΔΔΤCTGΔ	GGATTGAGCC	AACIGICIIC	CTTGCAGAAA
127/01	CCCACCCTGA	ATTGTGATCC	TACCTTTGAA	CIIGAGGAAA	IGATITIGGA
127/51	CTCCAAACCT	CTACATAAGA	AAAAAAAGCG	ICIGGCAAAG	AAGGAGAAGG
127501	ATATCACCAA	ATGCGATTCT	TCTCAGGTAA	GCAGGTCCCC	ACCAMACTCA
137551	GGGTCATGGG	TATCCCCATG	ATGGCTGCAA	TATCTTCGAG	AGCITCIACI
137601	GGGAGGTCAT	TTCAGCTTCC	TGCTTTIGCT	GCTTAGTGAA	CTCACCATCC
137651	. TAGATCAGCC	GGGTTTCTAA	AAGGGCAGAC	CAGAGCTCCT	CTCCCATTAA
137701	. TAGCAGCAAC	ATTITACTIG	TAGGCTTICC	GTCTAGAGTT	ATTTACAAAT
137751	. CTTGACTCAG	TTATTTCTCT	CTICCAGITO	TCAATTCAAA	CCCATGATTC
137801	. TTCCTGGGAG	AGGAACTGTC	ATTGGCCAAG	CTTAGGTCAG	TECTTETTT
137851	. ATAAAATTAT	GGTAAAGGGG	CAGGIIICAA	AGTACACACA	ACCCTAGAGA
137901	GGACCTCACT	CCTGCTTTGA	GGAGIIICIG	GGAGCAGCCA	ACCCTAGAGA
137951	TGATGTCTGT	TCTTTGCCAC	, AAGCAGAATI	TTATGATATC	GTGGAGCACT
138001	GAAGAGIGIC	TIGHTCACAGG	AATGACGGAA	TTCTAACATG CTTTGTAACT	AAGTATATTA
138053	ATTGCTGGAT	CACTCACACA	TCACATTTCA	GTGAAGTAAC	TTGCAAACAC
138101	LTICICIGICA	GAGTCAGAGC	CATCTCCCTC	TATGAATTAT	AATGATGATG
138151	LICAGIAGGAI	CTTACTTTC	CTCTAAAGG	CATCTATCTA	TCCACACGAC
13820	L AAGTAATAAA	CCTCCATCA	TCCCTCCCT	CCTCCATCCA	TTCATTTAGG
13823	CTACTTTTT	TTACTACCT	TGATCTGCC	GGTCCTGTGC	TAAAGACTGG
1202E	L CIACITITI	CATTGAGAT	TAATTTCTA	ACTCAGTGCT	GTCCCTTTTC
1303D.	L AGIGAGAAAI	TETACTET	TGGTAAAGA	GGCTCTGCAA	ACAAATAAGT
12040.	L ICAAAGAIIG	TCCTTAATT	r CTCTAGTAG	CAGGGGCCAC	TATATATTC
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12055	1 TCCCTTCTCC	: ΤΓΔGΔΤΤΓΓ	C TTCAGGAAA	T ATTITICIAGO	ACCUTCCAAG
13860	1 GAATGCTTAG	CTGTGCTGC	T AACCCGTCT	T GCATALIGCT	IGICICIGAA
12065	1 CTCTCTTCTT	· CCCAATGGT	C TGTTCCTCA	T GAICAIGICA	IAACCAACCC
12070	1 CCTTCTCCAG	· ACTTGCTCC	T TCCCCTGAC	C TAGCAGAACT	I GGC I CAAGG
12275	1 ΤΕΚΑΤΑΓΑΚΟ	: CCTCTCTGA	T AACAGGACC	I AACA IGIGA I	AAAAACCAAG
12220	1 AGATCCTTTT	ΓΤΔΤΤΔΓΔΑΘ	T TTTTAAAGT	IIIAGAAAIAA	CIGAGCAATI
12005	1	ʹͺͳͳͳͳϾΔϹϹϪ	T ACGTACCAT	G CICAACAIGA	LICIGCCCAIC
12200	1 TTTCCTGCC/	CATCCTTGT	<b>A CTATCCCAC</b>	T CTGACCCICA	CITAAAACCC
12205	1 TCCAACCTCA	\ CAGGCCCTG	C AAGTGTCTC	A CICICAAGC	A CIGAACCIII
13000	1 TOTTOTTOT	r caaggcctt	T GCCCTTGCT	CTICCCIGIIC	. CIAGAAIGGI
12005	1 CTTCCCTTT	^ ΔΤΟΤΤΟΔΟΔ	T AGGGGGCTT	CCICICALIC	HATACCHA
12010	1 AATATCACC	r TGTCATTTC	T GTTGTTGAA	T TATAGGAIG	I IIIIIACATA
12015	1 TTCTGGATA	r τασΔCCCTT	A TCAAATATG	I GAACIGCAAA	A INGILICIC
12020	1 CTTACTCAT	τ στασσαασσ	C AGCATTACC	C TGATACCAA	A CIGGACAAAG
12025	1 ΛΟΛΤΟΛΟΔΑ	Δ ΔΔΔΤGΔΤΔΔ	T TACAAACTG	A CAICIGIIA	I GAATATAGAT
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12025	1 AGATGTTTC	τ τατιτιτΔ	A TATTGGTGT	TIAIAGCIAIA	A AAGIICCIIC
120//	1 TCACCACTG	ς σττοδοστά	T CCCATAAGT	I IIGGGAIGC	i Giggiiigii
13945	1 TTTAATTCA	T CTCTAAGTA	A TOTGATA	I CICAIGIGA	т ттстстттт

139501	GACTCTTTTT	TTAAGAGTTT	GTTGTTTAAT	TTCCACATTT	TTGTGAATTT
139551	TCCAGTTTTC	CTTCTGTTAT	TEATTCCTAC	CTTCATTCCA	ATTATTTCAC
139601	TCTTTTTAAA	TTTTTTCATA	CCTCTTTTCT	COTTACCTTC	CATCCTTTCC
120651	TTTAACTCTC	ACCATATTCA	ACACCCTTCT	GGTTTCCTTC	CATGGTTTCC
120201	TTTAACTCTG	AGCATATICA	AGACGGIIGI	TTTAAAATCT	CACTCTAGAA
139/01	AGCTCAATGT	TTGAGCTTCC	TCAGGACAAT	TTCTATCCGT	TGATTTTAAG
139/51	TCTTTGAATG	GCAATATTTT	CCTGTTTCTT	TGTGTGCCTT	GTGATTTTTT
139801	TTCTGTTGCT	ATTGAAAACT	CGACATTTAA	ATATGATAAT	GTGGTAACTC
139851	TGGAAATCAG	GTTCCTCCTT	TCTTCATGGT	TTGCTATTTT	TTGATTGTTG
139901	AAGGCTGTAG	TTATCCATTG	TTTAGCGACT	TCTCCAAACA	ATGTTTGCAG
139951	AGATTGTCTG	CTTTCTTCTC	TCATCACTCA	ACTITCICIT	ACTITACCCT
140001	GTGCTCAGCT	AATCTTTTCA	CTCACACTTA	ACACCAACAC	CATTITAGCCI
140001	TTCTCTCAGCT	AATGITTGA	CIGAGATITA	ACACCAAGAG	CATTITIAAG
140001	TIGITITICT	TITCHAATI	IAGIGITCAC	TIGGTICCAG	TAAACCTTTG
140101	AGTGCTTTCC	GGAGTTTTGA	CAAAGTTGGT	TTTGACAGTA	TCTGCTTGTT
140151	TTTTTGATGT	TTCTGTTCAG	AGATGGGGCT	TGGAACTGCT	TACATCAGCA
140201	TTTTTCTCTA	GATTCTTCTA	ATCTTGTACC	CCAGGTTCAA	<b>AAATAAAAGG</b>
140251	TACTTTGCTT	CAAAACAAAG	AATAGTCTTT	CTTCCAAGAA	GAATCAGAAA
140301	GATTATGAAC	TATTTTCTG	ATTCTTCACT	CTATTTTCTC	TCTTTTACAT
140351	TAAGGCTTTT	AAAACATGAG	TCAATCTTAC	CTTATTATAT	TATTAACATC
140401	CTCGTTCATT	CATTCATTCA	TTTATTCACA	TCACTCTAAA	ATTCCTCCTT
140451	TGTTAGGAAA	TATTTCTCAC	TACCTCCTTA	ATCCTATCCT	TACATACACA
140501	AACTCCTCTC	CCAATTCCTCAC	ACTOCACOTA	AIGCIAIGGI	TAGATACACA
140501	AAGTGCTGTG	GGAATIGCTC	ACTGGACCTG	AGTGAAGGGT	TAGGATAGGC
140551	TTTCCAGAGG	AGGCAACATT	TGATCTGGTT	CCTCCAGATT	GAGCAGAGGT
140601	AGGTGAGCAT	ACAGGAAAGG	ACAAGAGCAT	TTCAAGGCTG	GCACATCTCA
140651	GGGCACAGGC	AGATCTTAAT	GTTACAGAGG	<b>AAATAAAATG</b>	ACAGGTGGTT
140701	TCTGATCATA	GGAATTACCC	ATGCTGTGTT	CAAAAGGCTT	GTGACATTAC
140751	TCATCCTCCC	TGCCTTTAGT	CTTATCTAGA	GCCATTCACT	GAAGGCATTC
140801	CTTCAGCAAA	ATCTAACAAG	ΔΑΓΑΤΑΓΑΓΓ	ATATCAGTAT	CATATTACCT
140851	ATAGCTTAGC	CCCATTTCTG	CCCCACTGTG	TCTACCTCAC	ACTCACCTTC
140901	TTACTCTAGA	CCCATTICIO	TCACTCTTTA	CCTACCCACA	AGICACCIIG
140051	CTCAACTCTT	CCCAAATTCA	TCACIGITIA	GGTACCCACA	TTAGAAAAGA
141001	GTCAAGTGTT	GGCAAGGGAA	TICCAATCAA	GCCACAAGCC	TGGAAAAGGA
141001	GCTCTCTATT	CIGAGCICIC	TGAGTTCTCT	ATTCTGTTTA	ATTGGTCTAT
141051	GCGTCTGTCG	TTGTACCAGT	ACCATGCTGT	TTTGGTTACT	GTAGCTTTGT
141101	AGTATAGTTT	GAAGTCAGGT	AGTGTAGTAG	TGTAATAATG	CCTCCAGTCT
141151		1111111111	TITTITITI	TITITITI	<b>GCTTAGGATT</b>
141201	GTCTTGACTA	TTCAAGCCCT	TATTTGGTTC	CATATACATT	TGAAAATAGT
141251	ттттст	AATTCTGTGA	AGAATGCCAA	CAGTCATTTA	ATGGGAATAG
141301	CATTGAATCT	ΑΤΔΔΑΤΤΔΟΤ	TTAGGCAGTA	TEECCATTIT	TATCATATTC
141351	ATTCTATCTG	GGAACCTGGA	ATCTTTTCC	ATTTCTTCT	CTCCTCTCTC
141401	ATTTCCTTGA	CCACTCCTTT	CTATTTCTCC		
141401	CCTTCTTACC	TATATTCCTA	CCTCTTTAT	TTGAAGAGGT	CCTTCATTIC
141471	CCTTGTTAGC	TATATICCIA	GGIGITIAL	IGITIGIAG	
141501	TGGGAGTTCA	TICATGATTT			TTGGTGTATA
141551	GGAATGCTAG	CAATCTTTGC	ACATTCATTT		GTTTCAGTAT
141601	TTTAAAAAACT	TACTTCAGGT	GATTCTATGT	GTGCAACCAT	GATTGAGATA
141651	CACTGTTATA	GAATCTAGGA	TGTGATAAAC	TAGAAGAACA	TAACTAAAGT
141701	TTTGCATTTT	TCGGGTGTCT	CAGTTTCCTC	ATTTATAGAT	GGAGTTGGTA
141751	TGTGTACCAA	GTTCATAGGC	TTGTTCTGAG	TAAATTAGTG	CATGTAAAGT
141801	GCTCCACAGA	ATGTTAGCTG	TTGTGATGCT	TTACTTTCCA	TTGCACTTCC
141851	TGACTCCTAG	CCTITCTITT	CCTTGGCTCT	TTTTATECTC	ATGTCAGATG
141901	CCTCTATTGT	TTCTTTCCCC	CCAGAATATC	CTCCACTTTA	TOTTCCTCTC
141051	CTCAACATCT	TTAAACTATA	CAATCAACAC	ACTCCCATTIA	CACCCACTCT
142001	CTCTCACAAT	TCACCCAAAT	GAATCAACAG	ACTUCCATUC	CACCCAGICI
142001	GTCTGACAAT	IGAGGCAAAI	TCCCTAAGTC	CICHIGHTCH	CCTTCTGAGA
142051	TTTCCACCTG	CTCTAACCCC	TTCCAATATT	TCAGATGCCG	TCTCCAGCTA
142101	TGATAATTTA	ATCAGTGTTT	GCTCTGCTCA	TCCTTGATAT	GTGAGTCCTA
142151	AGATTTTAAG	CGATCATTTC	CCTTCTAAGT	CATGTATGAC	CCATTAGTCC
142201	CTCCATTCTT	TTTTCTTACC	CCTCATTTCA	TATTCTCTTT	ATGGCTACTC
142251	CTGTTGATGT	ATCCATTTGG	CCACACTTCT	TAAACTTCTC	CACCTAAAGC
142301	AGAGGAAAAA	GAACAAGTTG	AACATGAACC	CTTTAAGGGT	AATGGGGTCT
142351	GAAGTGTCAC	ACTAAAAGGT	CATCTCCAAC	TATCTATTTC	ATATCTTCT
142401	TTAAATAAAA	TAGTTACATA	CTACACCCAA	AAAAAATCCA	TCTCCATTT
142451	CCATTTCACT	CAATTATAAC	CTTCATTTTT	AATCCTAAA	ATTATTAT
142501	GCATTTCACT	CCCCTAAAAC	TOTTCOTCO	AATGCTAAAA	ALIALITIC
142701	CTAAAATCTT	GUGGTAAAAG	TGTTGCTCCA	AAGAGCTTTT	ATCAGATTAT
146331	GTTTATCCTG	TAGCTGCCTG	TCCCCTGTGA	CCGATACTGG	AAACCCTCAG

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142951 AAGTCATCAA TAGATGTTGAA AAGCAAATA AAGAAGGCTC TGCTGACTAA 143001 CTTTGCATGT CTGCAAGAAA GTCACAAATA AAGAAGGCTC TGCTGACTAA
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143101 TATCAGGATT CAGTATAGAG AGATAAAT ACTAGCTTTT AGATTAATTG 143151 GTAGAACCTC CAAGCTACAAT TTACCAATAAT ACTAGCTTTT AGATTACAA
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443364 CTACCCACAC CTTTAIIII   {  GIAIAGII     LAAGIIACI   GICICOIO.
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A ASSET COTA ACCCAR CACASTCTCT TC-ASTILLAGIS AGGAGGGGGGGGGGGGG
4 43004 -CACACCATC CCACTICALL (LABIN 1996 LAACAUAUCA 7079'9'9'9
AAROET ACAAAAAAA AAAAAAAAAAAAAAAAAAAAAAAAAAA
4 4 4 6 6 4
4440E4 CCTCATCCCT TTCACCTATC ALLICILIAA GIALICIGII IICCIIIII
4 4 4 E 4 T C C T C T T C C A T A C A T T C C C C
144151 IGGIGITECA TACATTECTO TAGGECATO ACATAAAATA 144201 CCTGGGCCAC GTTGGAAGAA GAGGAATTGT CTTAGGCCAC ACATAAAATA
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144301 AATCICCIAA IGITTIAAGA AAGTTACAT GGCTGTGGGT TGGACAAGCT 144351 AAAGCCATCC TGAGGCACAT GTGGCCCATG GGCTGTGGGT TGGACAAGCT
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14451 AGACTCAGTA ATTICCACTG TECTGLEACE CTGTAGCAAA TTTTTAAATT 144501 CCTTGCCTGC TCAATTITGC CGTTGAAACC CTGTAGCAAA TTTTTAAATT
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144651 IGATTTICTC TATATCTTCC TATACCTCT GTTAGGTCTT TTTAAGGGAT 144701 GTTTTGATGT CTTTATCTAG TAGGTCTAG ATGAGCCATA CTTCTCTATT
144/01 GTTTGATGT CTTTATCTAT TAGACCCATA CTTCTCTATT 144751 AGGTTTTTTG GTTTATGTTT TTTACTGTGA ATGAGCCATA CTTCTCTATT
144751 AGGITTATT TITTGTATTG GACACTTGAA TCTAATAATG
144801 TCCTGGCATG CCTTGTTATT THETTET ATCCCCAGGG TTTGCTGTTT 144851 TGATAAATCT AGGAAAATCA GATTTCTCCC ATCCCCAGGG TTTGCTGTTT 144801 TCCTGGCATG CCTTGTTATT TATTGTTGTA AGCTGTCTCC
144901 TTIGITATIG TITTIATIT TATTORIA AGATETTETT AGGTETTTTE 144951 ATGCCAAGGA TCAGCTGAGG TGTAAACATA AGATETTET AGGTETTTE AATTTTECCT
A A E A E A A A A A A A A A A A A A A A
4 4 5 4 5 4 4 4 6 6 4 6 6 4 4 4 4 6 6 6 6
4 4 5 4 5 4
4 E 2 A 4 C C C A C C T C C A A C A A C A A C A A C A A C C A C C A C C A C C C C C C C C C C C C C C C C C C C C
A ARARA ARARA ARAA ARAA ARAA ARAA ARAA
4 ACOM ACTICITECT TICCACCCII. ACICICACAG GUIGIGIGGA AMENGENE
4 4 5 5 5 4 CA A CA T C T C C T C C T C N C C C C C C C C C
4 45 404 CCTACCTCCT CCTCTCCTAA (AA(-(     AA(-)     IIII   LAIAM     IVOC   UCUC
A A E A E A THROUGH A COCCA A COCCATTOCATA GARAGE LIGHT A AGULL LICHAL AGACTECTON
4 4 5 5 6 4 6 7 7 6 7 6 8 6 7 7 6 6 6 1 1 6 6 6 6 6 6 6 6 6 6 6 6
4 AFFE4 CCACCCCACA CACATTCCTG GIGGIIG III III IIICCMOC IICCCOUVII
445CA1 CTTCACA TACCATCCAT
145651 GGCTATTCAT TGAATAGACT GTCACCAGGT TATTGGCTGT TTGAAGATTC
TATANT COCINITION COMMISSION -

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145701 TCATTTGTCT GCTAACTATA CCTCTATTTT TTTTCTACGT TCACCTGGAA
145751 GACATGTCTT CTTCAAGAGC ACCTTGACTC TGTCCAGAAG GAGTTCATAA
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 147451 TTACTCTTTT TTTTCTTTTC AGGCAGAGTC TCACTCTGTC ACCCAGGCTG
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   148551 TTTCAGAGAA GGGGATG
   (SEQ ID NO: 3)
   FEATURES:
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   Start:
               2003-2054
   Exon:
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Intron:	40000-41067 41068-41219
Exon:	41220-79497
Intron:	79498-79500
Exon: Intron:	79501-86044
Exon:	86045-86218
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Exon:	105153-105190
Intron:	105191-113211
Exon:	113212-113301
Intron:	113302-123667
Exon:	123668-123765
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Exon:	132806-132922
Intron:	132923-133775
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Intron:	133849-134127
Exon:	134128-134155 134156-134530
Intron:	134531-134545
Exon: Intron:	134546-135588
Exon:	135589-135601
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Exon:	137398-137526
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Exon:	145752-145816
Intron:	145817-146200
Exon:	146201-146291
Stop:	146292

### SNPs:

DNA Position Minor	Major	Minor	Domain	Protein Position	Major	
210 332 1131 1221 2011 4309 4345 4651 5037 5126 6048 6229 6328 6350 6382 6434 6722 6751 6752 7070 7306	GTTCGACTACG - GCGAACATT	A A A T C C T C G T T T A T T - G T T C C	Beyond ORF(5') Beyond ORF(5') Beyond ORF(5') Exon Intron	3	A	Α

FIGURE 3WW

7339	Α	G	Intron
7531	G	Α	Intron
8902	Ä	Ğ	Intron
0302	2		Intron
9471	G C	A	
10023	C	Т	Intron
10594	C	G	Intron
11233	č	Ť	Intron
11733		; <del>-</del>	Intron
11295	-	A T	
11295 11534		Т	Intron
11757	T	C	Intron
11951 12901	G	Α	Intron
12001	č	Δ	Intron
12901	c	A T	Intron
13040	Ċ		Intron
13081	Α	G T	Intron
13173	G	Т	Intron
13272	C	T	Intron
13333	Ä	- G	Intron
13333	~	A	Intron
13485	C		
13933	Α	T	Intron
14086	G	Α	Intron
14094	C	T	Intron
14141	Ğ	<u>-</u>	Intron
14031	9	C	Intron
14831	T	C C G	
15319	Т	C	Intron
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15335	Α	G	Intron
15477	G	<u> </u>	Intron
134//		2	Intron
15650	Ţ	<u>_</u>	
15880	C	Ŧ	Intron
16944	G	A C T A T	Intron
17061	C	Т	Intron
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17642		•	Intron
17642	T	A	
17737	Α	Ĉ	Intron
18068	Α	G	Intron
18339	C	Т	Intron
19361	č	Ť	Intron
18361 19218		ĠТ	Intron
19210	A		
19298	C	A	Intron
19629 19679	C	T	Intron
19679	G	Α	Intron
19981	Α	G	Intron
20014	Ĉ	Ť	Intron
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20280		_	Intron
20612	Α	C	Intron
21966	C	T C	Intron
22017	T	C	Intron
28009	G T	Α	Intron
28059	÷	^	Intron
20039	<u>+</u>	A C	Intron
28580	T	ي	
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28823	-	A C	Intron
28827	C	G	Intron
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20044	2		Intron
30128	T	A	
30150	Т	G	Intron
30188	C	Т	Intron
30453	Ť	C	Intron
34990	À	Ğ	Intron
2E202	2	Ä	Intron
35203	G		
36206	G	<u>A</u>	Intron
39692	C	Т	Intron

40095 40191 40287 40384 40510 41664 48324 48423 50015 52623 52773 53140 53848 57693 53848 63478 63478 63478 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165 71165	ATGTGCTCATACGGA - ATTAGCACGAACGTGACGAC - AGAGC - ACGGAATGATGGTAC - ACG	GCACATGTCGGGGAATATCCTAAGTAGGTACAGGAGTAGC-T-GTTAAGGCATAAAACTACTT	Intron In
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106378	Т	G	Intron	
107310	C	Т	Intron	
108663	Ċ	Α	Intron	
108876	A	T	Intron	
110733	Ċ	G	Intron	
111546	Ā	G	Intron	
116728	Т	C	Intron	
118403	G	Т	Intron	
118491	C	G	Intron	
118888	Α	G	Intron	
125444	_	ΑТ	Intron	
125810	T	C	Intron	
126092	Ť	C	Intron	
127506	G	Α	Intron	
127878	Ğ	T	Intron	
139738	Ť	С	Intron	
140261	ċ	Т	Intron	
141590	Ť	G	Intron	
142613	Ċ	Т	Intron	
142774	Č	Α	Intron	
143288	Ğ	Α	Intron	
145610	Ä	Ċ	Intron	
148360	Ť	č	Beyond ORF(3'	)
<b>-</b> .0300	•	-	•	

#### Context:

DNA Position

[G,A]
CTTCCTTAGGGGTTTCATAAGTTCTTTTTCAATAACTCATCCTTAACACTTTCTCCAATT
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TGCCTGTAATCAATATTCCCTTCACATGTAAAGAGCTCAGGAGGAAATCAACTATTTTTT
[T.A]

### GGAAAGTACCATTATCTTCCCCAAGTTCAGAAGAAGAAAACAGAGAAAATATATTGAAATT

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  AGTTACTTTAAAGGACTCTAGAAAAACTAGGTTGAAGGAGAGTTAGGCTTAGGGACCAGA
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  [T,C]
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  CATGTGTCAAGATTCTCTTTTTTAAGTCTGAGTCGTATTCCATTGTATGGATATACC
  ACATTTTGTTTATCTTTTCATTAGTTGACATTGTCCTCACCTTTTGATTTTTGTGA
  ATAAGGCTGCTATAAACATTGGTGTGCAAATATCTGTTCAAGTCCCTGTTTTCAATTCTT
  [C,T]
  AGGGTATATACCTAGAAGTGGAAGCACTGGATCATATAATTCCTTGTTTGACTCTCTGAG
  GAACCATCATACTGTCTTCTACCTAATTATGCTTTGTGTTTTAGTAATGGGACACAGCCT
  GGCATGATGGGCTAGAGTATTGGAAAGGCATGCACAGGTTCAAGTCTCAGCTGTGCCACG
  TGCCAGTAATCTACATGTTTCTATGAGAAAGAGTCAAAGAGGATATAGCCTGGTCAACCAT
  TATCAGACACTGGAGTCAGTTTGACTAATTATATGGTGTTCTAAGGAAACTTGAGGTACC

TAAGGCTGCTATAAACATTGGTGTGCAAATATCTGTTCAAGTCCCTGTTTTCAATTCTTC

[A,T]
GGGTATATACCTAGAAGTGGAAGCACTGGATCATATAATTCCTTGTTTGACTCTCTGAGG
AACCATCATACTGTCTTCTACCTAATTATGCTTTGTTTTTAGTAATGGGACACAGCCTG
GCATGATGGGCTAGAGTATTGGAAAGGCATGCACAGGTTCAAGTCTCAGCTGTGCCACGT
GCCAGTAATCTACATGTTTCTATGAGAAGAGTCAAAGAGGATATAGCCTGGTCAACCATT
ATCAGACACTGGAGTCAGTTTGACTAATTATATGGTGTTTCTAAGGAAACTTGAGGTACCA

- TGGAAGCACTGGATCATATAATTCCTTGTTTGACTCTCTGAGGAACCATCATACTGTCTT
  CTACCTAATTATGCTTTGTGTTTTAGTAATGGGACACAGCCTGGCATGATGGGCTAGAGT
  ATTGGAAAGGCATGCACAGGTTCAAGTCTCAGCTGTGCCACGTGCCAGTAATCTACATGT
  TTCTATGAGAAGAGTCAAAGAGGATATAGCCTGGTCAACCATTATCAGACACTGGAGTCA
  GTTTGACTAATTATATGGTGTTCTAAGGAAACTTGAGGTACCACAAGAAAAGTCTCCAAA
  [T,C]
  CTAAATAATTACTAATGAATTAATTGAGGGGGAAACTTATTTAACCTTTGTAAGCCTCAG
  TTTCTTTGTATGTAAAATGCAGGTAATAATTGGGCATACTTCATTAGGTCTTTGTGAGGA
  TTGAATAAATAATGCAAGTAAAACACTTAGCAAAGTATTTCCCATAAAGTAACCACTCAA
  TTAATGCTAATTAAGTGTTATTTACTAACATCAGAGTTTCCTAGTGTGAACTCTTTGAAG
  TACTTTAAGTTCTGAGAAAAACAAAATTAATTAAATGCAACTCTGTCGATTCCACAGGTTA
- GTCAGTTTGACTAATTATATGGTGTTCTAAGGAAACTTGAGGTACCACAAGAAAAGTCTC
  CAAATCTAAATAATTACTAATGAATTAATTGAGGGGGAAACTTATTTAACCTTTGTAAGC
  CTCAGTTTCTTTGTATGTAAAATGCAGGTAATAATTGGGCATACTTCATTAGGTCTTTGT
  GAGGATTGAATAAATAATGCAAGTAAAACACTTAGCAAAGTATTTCCCATAAAGTAACCA
  CTCAATTAATGCTAATTAAGTGTTATTTACTAACATCAGAGTTTCCTAGTGTGAACTCTT
  [T, C]
  GAAGTACTTTAAGTTCTGAGAAAAACAAAATTAATTAAATGCAACTCTGTCGATTCCACA
  GTTAATTAGACCTATTCATGTTTCTATTGACTGGATTAACAGAACGGCAGATTTTATGGA
  TTCTGTTAAAACCTATATAAAAAACACTTTAAAAGAAGCCAAGTTATTGACTGCACAAAAA
  CATAATCTCATCTGATATCTTTTTTTATCCCCCTGAGGTTATTGTGTTTTTTTAAGGCA
  AAATCAAGAACTAATTGGGATGAAAATAACTAAAGTTTACTTTGTCTGATTTAAGTCCCA

FIGURE 3DDD

TGAAATAATTTTTGTGAAAAACATTTTAATGTCTGTGGCTCATAATATTCTGTGGATCTC
AGTTTGGGAAATGAAAGATTATAATCGTATCTACTCTTTATCTGTTGGAAACATCTTTCC
ATTTATTTTTCCTGCTGGTTTAATGGCAACAAATTTTTACATGTGAAATATTTGTAATGT
GATTTATATGAAAAAATGTAATTTTCTTATTACACGATCAAAAGTGGTTATGCTCCTCTG
TAAGTTTTTCCTTACAAGTTTTTATGTTGCATAATTTATATCTATTTGGTTTAATGAGTA

- 9471 GCATAATITATATCTATITGGTTTAATGAGTACAACACAAGATAGCTCAGTTTAATTCTG
  GGATGTTGGATGTTTCTAGTTAAAGTACAAGTTGGATTTGATGAAAATTCATTGCTTCTT
  TATGATTTTTTAAAACTCAAGAACATGTTAGTTAAAGAGTGTCTTCTGAACAAATTCTTG
  TGAAGTAGTTGCTGATTATTAAGTAACACTCATGCTACCGTAACTTTTTATACTATCCAA
  AGCTATAGACATTTTAATTTTCAACTTGCAACTACCTAGGTTGAAAAATTAAATCTGCA
  [G, A]
  GCCAGTTTCATTATTCAGACAATTTGGTTATCACTTCAAGCCTACTATCTTCAAAGAAAA
  TGGGAGTGCAGGCCTTCATGGGAGCTGACTTCTGCTGTATGGCCTTGCAAATGTCAACTC
  GATTAGAGTGACCAGTGTTAGCCCTCAATTCACAAACTCAGGTCCCATGAAATATACACG
  GATTTCTACTATGCATTACTATGTGACCATTCATGGAAGTTTCGTTTGGAAACACAGACA
  TTAAAAAGCCAGTCATGGAAATAACATTCTTGTTAAAACAGGACATTGGCAAAAAGGACTA

- CATCCAACAGTTGATCTCCCCCCATCCTGCCCCACTGTTCTACTTTGCAATTTGTT
  TGAAAGAAATTGTCAATATATTTCTGACTTCTGAGCAAATCCATGAATCGGGATCCAGCA
  ACAGGAAAAGAAGCTGTTGCTGCCCATTGCTTGGTTTTGGCACCAGGAATGGATAAATCC
  CAGACTTCCTGGGGCACGTGTTTTATAAAAGGGAAGTGCTGACAGCAACAGCTGCCA
  TCAATTGGCCTTGGAGACTACTTCCCTGGAGAAGCTCCAATTATATTCTTAAAGGACCCA
  [C,T]
  CAAGCTCTTCAAGTGTTAGTGGCAACCATTTGCTGCCAACCATTTGAAATGATGAAGTAA
  TTTTTTTTTATTAGTGGATCCTAAGTGATAGGCTCTAGAACTGATCTTCAACCTTAACTA
  ATATCATGGCATCAGAGGGCTACAGATTAAATCAGTGGTTCCCAGTCACTCTCTGTGGAC
  AAGTAGCAACTACGACAAAGCTTTTCTTAGTCTATGGTGGAAGAGAAAAATTAAGGACAAT
  GTAATAAGCATCCCATAAACTTATTAAAACCTATTAAAATTTAATTTTAAGATTATGTCAT
- AAAGAAATTGTCAATATTTCTGACTTCTGAGCAAATCCATGAATCGGGATCCAGCAAC AGGAAAGAAGCTGTTGCTGCCCATTGCTTGGTTTTTGGCACCAGGAATGGATAAATCCCA GACTTCCTGGGGCACGTGTTTTATAAAAGGGAAGTGCTGACAGTGCAAACAGCTGCCATC AATTGGCCTTGGAGACTACTTCCCTGGAGAAGCTCCAATTATATTCTTAAAGGACCCACC AAGCTCTTCAAGTGTTAGTGGCAACCATTTGCTGCCAACCATTTGAAATGATGAAGTAAT [-, A, T]
  TTTTTTTATTAGTGGATCCTAAGTGATAGGCTCTAGAACTGATCTTCAACCTTAACTAAT ATCATGGCATCAGAGGGCTACAGATTAAATCAGTGGTTCCCAGTCACTCTCTGTGGACAA

- CAGTGTGGAGACCAAGGAGAAGAGGAATCCTAATATTTAGAAACAAGGCAGTGGATAGCA
  ATCTAGCTATGGAAAGTGGAAGGAAAGAGATAGTTGATCATCCAGTTCAACACTACTCTT
  GTTGTAGTTCACTTATGTTGAATGCTTCTGTGTGACTAAGTCGGTGAGAAAAATCTATGG
  GAGTAGGCAACATGGAGGATGTTGGTATTCACAAAAGCAGTTTAGTGGAGTGTGGAGGCC
  TGAGCCAGACTAGAATGAGTTAGGAGTAGATGGAAGATAAGAATGCAGATATGGGCCCAG
  [C,T]
  GCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGTGAGCAGATCACAAGG
  TCAGGAGATCGAGACCATCCTGGCTAACACCCGTGAAACCCCATCTCTACTAAAAATACAA
  AAAATTAGCCGGGCCTGGTGGCGGGTGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCA
  GGAGAATGGCGTGAACCCCGGGAGGTGGAGCCGAGATGCCACTGCAC

#### 

CATCAACACCCACCTCCATATCCAGATATTGAGTACCTCAGGGAGTTCAATTTGGAAGCA 13933 AATGATGTGAAAATGTACTTTACTATCCAGTAACATTCTTGTTAGGGAGTGTTGGCAGAG ATTGTCGAACAACCATAATGCATTTTATCATTCGATCAGTCTACAATTTAAACATAGCAG GACTGGACAGAGGCACAGGAAGATTAAGCCACTGACCTTAAGTCAGACAGTCACATGGGT AGATCCGGAATCTTGATCTAAAATGAATACCATTTTTTCAGTTATAGCTATCTTCCCAGG [A,T]AAGAATACATCAAACACCCATTATGTGCCTAACTCTAAATCTTACTTTCAGAGAGCTAAA AACAATTTCATTTCACAGTGACATTCATCTTCGCTTCTGCCGTAACTCACATGCATATGC CTTAGACCACATTATTAATGAAGTATTGGGGGGTTCCATCTAGAGCACCTTTTCTTCCCT GGAGTTAATCATCCAGTTCAGCACCACTCTTGAGCTTTGCTTAGCTTCTTCTACCCATTT GATCAGTCTACAATTTAAACATAGCAGGACTGGACAGAGGCACAGGAAGATTAAGCCACT 14086 GACCTTAAGTCAGACAGTCACATGGGTAGATCCGGAATCTTGATCTAAAATGAATACCAT TTTTTCAGTTATAGCTATCTTCCCAGGATGGCCAACCAGAATGCATATATAAAATTTCAA AAACAAACATTGGGAATTGCTCTTCAGCAAGAATACATCAAACACCCATTATGTGCCTAA CTCTAAATCTTACTTTCAGAGAGCTAAAAACAATTTCATTTCACAGTGACATTCATCTTC [G,A] CTTCTGCCGTAACTCACATGCATATGCCTTAGACCACATTATTAATGAAGTATTGGGGGG TTCCATCTAGAGCACCTTTTCTTCCCTGGAGTTAATCATCCAGTTCAGCACCACTCTTGA GCTTTGCTTAGCTTCTTCTACCCATTTGGATTTTAAGGACAACAATTCCAATGGCCTTTA TCCATGTATTTAACAATTCATTATGAGCCAGGTGAAGTGGATCACACCTCTAATCCCAAC ACTTTGGGAGGCTGAGGCAGGTGGATCGCTGGAGCCCAGGAGTTCACAACCAGCCTGGGC TACAATTTAAACATAGCAGGACTGGACAGAGGCACAGGAAGATTAAGCCACTGACCTTAA 14094 GTCAGACAGTCACATGGGTAGATCCGGAATCTTGATCTAAAATGAATACCATTTTTTCAG ATTGGGAATTGCTCTTCAGCAAGAATACATCAAACACCCATTATGTGCCTAACTCTAAAT CTTACTTTCAGAGAGCTAAAAACAATTTCATTTCACAGTGACATTCATCTTCGCTTCTGC [C,T]GTAACTCACATGCATATGCCTTAGACCACATTATTAATGAAGTATTGGGGGGGTTCCATCT AGAGCACCTTTTCTTCCCTGGAGTTAATCATCCAGTTCAGCACCACTCTTGAGCTTTGCT TAGCTTCTTCTACCCATTTGGATTTTAAGGACAACAATTCCAATGGCCTTTATCCATGTA TTTAACAATTCATTATGAGCCAGGTGAAGTGGATCACACCTCTAATCCCAACACTTTGGG AGGCTGAGGCAGGTGGATCGCTGGAGCCCAGGAGTTCACAACCAGCCTGGGCAACATGGT CCACTGACCTTAAGTCAGACAGTCACATGGGTAGATCCGGAATCTTGATCTAAAATGAAT 14141 ACCATTTTTCAGTTATAGCTATCTTCCCAGGATGGCCAACCAGAATGCATATATAAAAT TTCAAAAACAACATTGGGAATTGCTCTTCAGCAAGAATACATCAAACACCCATTATGTG CCTAACTCTAAATCTTTCAGAGAGCTAAAAACAATTTCATTTCACAGTGACATTCA TCTTCGCTTCTGCCGTAACTCACATGCATATGCCTTAGACCACATTATTAATGAAGTATT [G,-] GGGGGTTCCATCTAGAGCACCTTTTCTTCCCTGGAGTTAATCATCCAGTTCAGCACCACT CTTGAGCTTTGCTTAGCTTCTTCTACCCATTTGGATTTTAAGGACAACAATTCCAATGGC CTTTATCCATGTATTTAACAATTCATTATGAGCCAGGTGAAGTGGATCACACCTCTAATC CCAACACTTTGGGAGGCTGAGGCAGGTGGATCGCTGGAGCCCAGGAGTTCACAACCAGCC ACAATTTATTTCATCATCATTGTCATCATCATTGTCACTGCTCACTCTTCAACATTTTTT 14831 TGAAGTTTTTGCCACTTTGATAACTTCTTCATTTTCTGTCCAGAGTATAACATACCAGGG AAAAGGCTCTAAAATAAGGCTTGAGGTATTAAAAAGATCTTCTGTTTAAGTCTTATGTTC CTAATCAATAACTAGAATTGGCCTGATTGCTTTCCTCAGTGGGTTTTCTGGTAGTCCTGA [T,C]ATGATATCGAGGCTGTCATATAGTCCTGAAATATCCTATCATTAACATTTGTGGTGGTAT CTGATATAAAGGTAGATGAACTTCATTGCAGCTATTCTTAGGAAATGCGTATTTAAATGC ATAGTTAAAAGCAAGATTTACAATTATAGAAGGAATGCAAATGAGTTGTAGAAAGCTCAT AAAATAAAAATCAAGAAGAAAGAATTACCCATCATGCCTCAGCCCAGTGATAACCACTGC TAATATTTTGGCTGTTTTCATTTGCAACCCCATCTCCATTCTAGCAGCCCTCATCCCTC AAATCAAGAAGAAAGAATTACCCATCATGCCTCAGCCCAGTGATAACCACTGCTAATATT 15319

## FIGURE 3HHH

TTTGGCTGTTTTCATTTGCAACCCCATCTCCATTCTAGCAGCCCTCATCCCTACCCA

CACTTGATATATCTGGGATGATATTCAATATACTTTTGTATCCTCATTTTCACCATAGGT AGTTTATGTCAATTCCTTGAAATTTGTTGATTTTCTTGAATAATTTAGCAGTTGTACAAT TCTAAAACATAAATATAATTTGCTTAAATATACATACCATTTTAAACATATTTAAATGTG AAAATACAGTTGAGTTCTCTTAGATTGCAATTTTGTAACTTTTTGATAATCCTTTGATCCT GAAAAAAATTTTTTTGGCATGAGGGAAGAGATGAATATTTCTTTTGGAGTATTTAAATCAT

15477 ATTATTTGTTAATTATGTTTTTCCTCTCACTAGAAAGTGAACTCCATGAGGGCCAGGGAT
TTTTGCTATTTTGTTCACTTTTGTATCCTTAGCACCTACTTTGTTGATTAAGTGAATGCA
TTAATGATCTATTTTTAATCTGTGTATGTGTATAAAAGACACTTGATATATCTGGGATGA
TATTCAATATACTTTTGTATCCTCATTTTCACCATAGGTAGTTTATGTCAATTCCTTGAA
ATTTGTTGATTTTCTTGAATAATTTAGCAGTTGTACAATTCTAAAACATAAATATT
[G,A]
CTTAAATATACATACCATTTTAAACATATTTAAATGTGAAAATACAGTTGAGTTCTCTTA

15880 AAAATTTTTTGGCATGAGGGAAGAGATGAATATTTCTTTTGGAGTATTTAAATCATCTCT
GCAATAATCCTTTGATCCTGAAAAAAAATTTGTGGCATGAGGGAAGAAGAATATTTCT
TTTGGAGTGTTTAAATCATCTCTACAATTAATAATATCTAAAGCAGTTTGGTTTGATTTAATTTTAAGTAGGAGATTAATTTTCAGTATGAATATTATTTAAAAAAACAAATATAGTCAGTTGAAT

TGCTGTGGAGGTTTCTGTACGATTTACTCAAAGCTGGCTCTTTTTCTGTACGCACTACCA
[C,T]

GCCCGGCTAATTTTTGCATTTTTTGGTAGAGATGGGGGTTTCACCATGTTGGCCAGGCT GGTCTTGAACTCCTGATCTCAAGTGATCCACCCACCTCAGCCTCTCAAGGTGCTGGGATT ACAGGCATAAGCCACCATGCCCAGCCTGCATTTATCCTTACATGATGGTGAAAAATAATG TTTGTACTTCCTTCAGAATAATTTCAAGAAGGATCCCTGGAGTCAGCTAATGATTAGAGT CAGGACTGTGCCTTAGTTGATGGCCCATATAGCACTACTGAACATGCCAGAGCTTTTGCT

- 17494 CTTTATGAGGAAGTTACGTTTAAAAGTAGAAGGCAGGCTGGGCGCGGTGGCTCACGCCTG
  TAATCCCAGCACTTTGGGAGGCAGAGGTGGGCGGATCACGAGGTCAGGAGATGCAGACCA
  TCCTGGCTAACACGGTGAAACCCCGTCTCTACTAAAAATACAAAAAAATTAGCTGGGCGT
  GGTGGCAGGCACCTGTAGTCCCAGCTACTCAGGAGGCTGAGGCGGAGAATGGCATGAAC
  CCAGGAGGCGGAGCTTGCAGTGAGGCGAGATCCTGCCATTGCACGCCAGCCTGGGCGACA
  [G,C]

AATATGCCTTGGCTTAGTAGTTTTGCTTCATTTTCCAAAAGAAGAAGCTTCTCTGGATAA GGTGGAGGTTAGTTAAGGGAGGTTTCAGTAAGTGACATTTTTATGAGCCTCTGCATCTAC TTACGGATGCACAGTATGACACAGCACCCGACAAGAATAAGTCCACCTATTACGGCTGCG AGGGAAGTAAGAATTGAGGCTATTATTCCTTCTCATTTACCAAACTACTTTTCTAGCCAT CTTATAAAGGGGTCATTTACCCCTGAGTTGCTGGCTAACTTATTGGATAGAGCAGTCAGA

FIGURE 3JJJ

CATTTTTATGAGCCTCTGCATCTACTTACGGATGCACAGTATGACACAGCACCCGACAAG
AATAAGTCCACCTATTACGGCTGCGAGGGAAGTAAGAATTGAGGCTATTATTCCTTCTCA
TTTACCAAACTACTTTTCTAGCCATCTTATAAAGGGGTCATTTACCCCTGAGTTGCTGGC
TAACTTATTGGATAGAGCAGTCAGACCATGCAGTGCCTTTCTAATACTTCCATTAGGGGC
AGTGTTGTTTGGGATGAAGGTGCAACATTGAGTTTTAATTATGATGCAAACTACCCCTCT

18068 GATGCACAGTATGACACAGCACCCGACAAGAATAAGTCCACCTATTACGGCTGCGAGGGA
AGTAAGAATTGAGGCTATTATTCCTTCTCATTTACCAAACTACTTTTCTAGCCATCTTAT
AAAGGGGTCATTTACCCCTGAGTTGCTGGCTAACTTATTGGATAGAGCAGTCAGACCATG
CAGTGCCTTTCTAATACTTCCATTAGGGGCAGTGTTGTTTGGGATGAAGGTGCAACATTG
AGTTTTAATTATGATGCAAACTACCCCTCTTTCTGCTACTATCATGTCTAAGGCTATTTT

[A,G]
TTTTGCCAAGCCATCTGGCTAGTAGCCCCTAATTGCTCAGCTATTCCATTAACAGCATCT

- 19298 TCTCAGCCTCCGAGTAGCTGGGATTACAGGCATGCACCACCATGCCTGGCTAAGTTTGT
  ATTTTTAGTAGAGACGGTGGTTTCTCCATGTTGGTCAGGCTGGTCTTGAACTCCCAACCT
  CAGGTGATCCCCCTGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGAG
  CCTGACCTGTTTTAAGTCTTTAGTTTTTACAATAGCTATCTTGGTCTTGTTGTTAGATGG
  AGGAGGAGCAACTGTTCCGTTGTGAGAGGGTTTTGGAAGAAGGCTTACAGGAAGGTGCAGG
  [C,A]
  GGTGGGGATCAAAGAAATGCATTTTAAATAATCTAATAGGGTTTGTCCCTGAAACCTCAG
  CCCCTATAGCATAAAACTGACTTAAAGAAGGGAACTGGCTTAGAAAAAGGGGAAGAAATTT

GAGAGTTTGAGATAATAACCTGTAGAGAATTATAGATAATAACCTGTATAGGTTTAGCTG ACAGCTGGGGGGGGGCTGTCTCTTTAGTAAAATGAGTGTATGGTTTTAGTAAATTACAA AAACTGGTTGGGGCAATCCCTTCTTGCTATTTAGTGGTCCACAGAACATTGGACCAACTA

- CAAATCCCCACAGGGTATAACAAGGCAAGCATTAAGTGCAATAGTTTGAGGCAAAATTGA
  CTTGGTTATGTTAATAACTAGATGGTCAGCAATAGAGCCAGTAAAGAAGAAAAGAGTAATA
  GAATAGATAAAAGAGAGTTAAATTTTTCTTAGCTTTAGTTTGGCAGGGCTTTCCCCTGGG
  GCTGTGGCCCACAACTCTGGAGGGGGCGCGCGTTTCTTGACTCGGGTGTGATGAGTCCAT
  [C,T]
  CCTTTTTCACTGTAGAAACAGCAGTCTTGGTGGTGAGCACAAGGTAGGGTCCTTCCC
  AGGCTGGCTCGAGTTTTCCTTTTCCACCCTTTGATAAGAACGTGATCTTCAGGCTGGT
  GTTGGTTTACCGGAAATTCTAGGGGTGGTACCTGTGCTAAAAGACTTTTAGTTTTGAGGG
  AAAGGAAAATGGAAGATAAACCAAGTATATAATTTCTAAGAAATGGACCTTTTGTTTTAA

GATGACAGTCAGGAGGCACAGAGGTATTTTTTCTGAAATAGAGAGGTGTCTTTGACTTGG

20014

## CTTTTTAACCTTTTATAATTTTTGTTAAAGAGCAGGTTAGTGCTTTAAGAAATACCTGTT

# FIGURE 3MMM

CCCAAATCCATCCTTTTTCTGTAGAACTTTAATGATGATACCTCATTCCTTTGTAACTTA 28580 ATTTTAAAAAGTTAATTATGCACCTACTATGATACGTCCAAAATGTTTTTAGGTGATGTG GATATAGCGAAGAACAAGACACCCAGTGTCTTCCTTCATGGAGTCTATATTCTTGGCA CATTGGCTGGGCGTGATGGCTCATACCTGTAATCCCAGCACTTTGGGAGGCTGAGGTGGA GGATCACCTGAGGTAGGGAGTTCAAGACCAGCCTGATAACATAGAGAAACCCTGCCTCTC CTAAAAATACAAAATTAGCCAGGCATGGTGGTGCGTGTCTGTAATCCCAGCTACTCTGGA GGCTGAGGCAGGAGAATCACTTAAACCTGGGAGGCAGAGGTTGTGGTGAGCCGAGATTGT AACCAACAGGCAACATTCTGGGCTGAAACAAAGGTAATTCATCTGGTAACAATAGCAATA TTTCTGTAGAACTTTAATGATGATACCTCATTCCTTTGTAACTTAATTTTAAAAAGTTAA 28595 TTATGCACCTACTATGATACGTCCAAAATGTTTTTAGGTGATGTGGATATAGCGAAGAAC AAGACACACCCAGTGTCTTCCTTCATGGAGTCTATATTCTTGGCACTGTTGGTCCTGTGT GAAGTCCTAACATTATTTTGCTTAATGTTTTGGCAAGAGAGGCAACATTGGCTGGGCGTG [A,C]GGGAGTTCAAGACCAGCCTGATAACATAGAGAAACCCTGCCTCCCTAAAAATACAAAAT TAGCCAGGCATGGTGGTGCGTGTCTGTAATCCCAGCTACTCTGGAGGCTGAGGCAGGAGA ATCACTTAAACCTGGGAGGCAGAGGTTGTGGTGAGCCGAGATTGTGCCATTGCACTTGTA TTCTGGGCTGAAACAAAGGTAATTCATCTGGTAACAATAGCAATAACATAAATAGCAGTA TGGCTGGGCGTGATGGCTCATACCTGTAATCCCAGCACTTTGGGAGGCTGAGGTGGATGG 28823 ATCACCTGAGGTAGGGAGTTCAAGACCAGCCTGATAACATAGAGAAACCCTGCCTCCCT AAAAATACAAAATTAGCCAGGCATGGTGGTGCGTGTCTGTAATCCCAGCTACTCTGGAGG CTGAGGCAGGAGAATCACTTAAACCTGGGAGGCAGAGGTTGTGGTGAGCCGAGATTGTGC [-,A,C]CAACAGGCAACATTCTGGGCTGAAACAAAGGTAATTCATCTGGTAACAATAGCAATAACA TAAATAGCAGTAATAATTATACATTATTGAGTTCCTATTCTCTGCCAAAAATGGTTGATA AGCACCTTTGATATGGCTTATTTTACCTAGTCCTCATTATAACCTTAGAAGGTATATTGT ATCTGGTCAAAATTGAAAGAAGAAATTGAAACTCACAGAGGGTAAATAATTAAAGTTCAT AGCTAGTAAGTAGTACAGACAAACCCAAAAGCAGAGTTTCATGCTCATAGTCACCATAAT 28827 CCTGAGGTAGGGAGTTCAAGACCAGCCTGATAACATAGAGAAACCCTGCCTCTCCTAAAA ATACAAAATTAGCCAGGCATGGTGGTGCGTGTCTGTAATCCCAGCTACTCTGGAGGCTGA GGCAGGAGAATCACTTAAACCTGGGAGGCAGAGGTTGTGGTGAGCCGAGATTGTGCCATT [C,G] AGGCAACATTCTGGGCTGAAACAAAGGTAATTCATCTGGTAACAATAGCAATAACATAAA TAGCAGTAATAATTATACATTATTGAGTTCCTATTCTCTGCCAAAAATGGTTGATAAGCA CCTTTGATATGGCTTATTTTACCTAGTCCTCATTATAACCTTAGAAGGTATATTGTATCT GGTCAAAATTGAAAGAAGAAATTGAAACTCACAGAGGGTAAATAATTAAAGTTCATAGCT AGTAAGTAGTACAGACAAACCCAAAAGCAGAGTTTCATGCTCATAGTCACCATAATGTAT 28842 TCAAGACCAGCCTGATAACATAGAGAAACCCTGCCTCTCCTAAAAATACAAAATTAGCCA GGCATGGTGGTGCGTGTCTGTAATCCCAGCTACTCTGGAGGCTGAGGCAGGAGAATCACT TAAACCTGGGAGGCAGAGGTTGTGGTGAGCCGAGATTGTGCCATTGCACTTGTACTCCAG [G,T]CTGAAACAAAGGTAATTCATCTGGTAACAATAGCAATAACATAAATAGCAGTAATAATTA TACATTATTGAGTTCCTATTCTCTGCCAAAAATGGTTGATAAGCACCTTTGATATGGCTT ATTITACCTAGTCCTCATTATAACCTTAGAAGGTATATTGTATCTGGTCAAAATTGAAAG CAAACCCAAAAGCAGAGTTTCATGCTCATAGTCACCATAATGTATTCAGAAACTTTTAGG GGCCAATGAATCTGAATTTAAAAACATGTATTTGTGTGATTTTGATGGGTGGACACACTT 30128 GAGAATCACGTCAGGACCATTTATGTGGCTCTCAATTACATATACACTACTTTATATTGC

AGTTGTTTATTTATGTTATATTGCAGTTATTTATTTATGTTTCATCTTTTTCCTGAGAA ATTACCTTCCTGATAATCCAATGCAGAGATAAATTAAGAAAATCTGTAGGAAAGAATAGA TCATCAAGTCCCTTGCAACATTCTTCTGAGGTTGTAATAATCTCCTCTAGGATGCTTTGC [T,A]

CTTTTCCTGCTACTTTCTCCCATTACAGGTCTCCCTACGGCAGCACTGCTTATATCACTT GGAACTTGAATCTATTTTGGTAAAAAAAAAGTTAAAATTAAATTATCAGAAGGATATTG GGGATGCCTGCAGAGTAATCAAAATAGGATCTATATTGTTATAGAGCCAGGCACATTAAT GCCATCAGCTTTAGCCCTTTATGTTGTGATTTTACTTTATTCCAAATGTCAGCTTTATCC TGTTGGATGTGCTGATCTTTTTTCTCTACATTCAGCCAGTTCCATTCTCATGTTCTGGAA

30188 GAGAATCACGTCAGGACCATTTATGTGGCTCTCAATTACATATACACTACTTTATATTGC
AGTTGTTTATTTATGTTATATTGCAGTTATTTATGTTATGTTTCATCTCTTTTCCTGAGAA
ATTACCTTCCTGATAATCCAATGCAGAGATAAATTAAGAAAATCTGTAGGAAAGAATAGA
TCATCAAGTCCCTTGCAACATTCTTCTGAGGTTGTAATAATCTCCTCTAGGATGCTTTGC
TGGATTTCCCTGGACTAGGTTGTCTTTTCCTGCTACTTTCCCCATTACAGGTCTCCCTA
[C,T]

30453 TTTCCTGCTACTTTCTCCCATTACAGGTCTCCCTACGGCAGCACTGCTTATATCACTTGG
AACTTGAATCTATTTTGGTAAAAAAAAAGTTAAAAATTAAATTATCAGAAGGATATTGGG
GATGCCTGCAGAGTAATCAAAATAGGATCTATATTGTTATAGAGCCAGGCACATTAATGC
CATCAGCTTTAGCCCTTTATGTTGTGATTTTACTTTATTCCAAATGTCAGCTTTATCCTG
TTGGATGTGCTGATCTTTTTTCTCTACATTCAGCCAGTTCCATTCTCATGTTCTGGAAGC
[T.C]

TTGAGACAGAAGATGGTAAGTGAAATAAAACAAAGGAAATAAAAAGTATCACCTGG GTTTCAGAATCAGCATGGTTTATGCTAAGGGAAAGACTTGGAAACCTTGATTCAACATAT AATTCTAAAAAGAGACAGGAAGAAATCCCACCTTGTTTCCTCTGATTCTACCTTTGGGAT GGGTAGGTATGTTATACAATAAGAATAACATTGAGATGACTGCTATAAAAATAGTGGTTA AGAGCCTGGGTCCAGAATGAGAAAGGTGGATATTGAATTTACCTGAGTGCAACTAGGCAG

35203 CTGAAATTCCAAGCATCAGGGTGTTATAACAGACTCTAAAAAGGGTTTCCTTTTTTCTTT
CCTTTAACATTGCTTATTGCACAGCATATTGAGACAGAAGATGGTAAGTGAAATAAAA
CAAAGGAAATAAAAAGTATCATCACTGGGTTTCAGAATCAGCATGGTTTATGCTAAGGGA
AAGACTTGGAAACCTTGATTCAACATATAATTCTAAAAAGGACAGGAAGAAATCCCACC

TTGTTTCCTCTGATTCTACCTTTGGGATGGGTAGGTATGTTATACAATAAGAATAACATT

[G,A]
AGATGACTGCTATAAAAATAGTGGTTAAGAGCCTGGGTCCAGAATGAGAAAGGTGGATAT
TGAATTTACCTGAGTGCAACTAGGCAGACTCAAGTGAGTTTTTACCCACTCCAC
TCAAATACTGGGTATGGCTTTGCAAAAACATTCAACCAGTTATCCACATAGTTGGTCTTA
ACTTTCCATGTGACTATAATGAATATAAACTTGCTAATGAGCAGAGTGATTTTAGTGT
TTAAACTATTTTTTCCCGAATAATAGTTCCTAGATGCAGTTAATGAGCCTTATTGGGTAC

AAAATTGAAATTACTTAGATACAAAAGAGTGGTTGTAGTAAGAAAATAGGCAAGGAGAAC
ATTITAAAGTGCTGATCCTCGGTAAAGCCATACATAGGATGCACCTTGGGAGCAGATCTTT
CTGAAGTCATTCTGTGCTCAGAGATGTTTCTCCTTACCTTGCTGCCTATGTCAAATTCTC
TGTGATATGTTCTTAGAGCCCCATGACCTCTCTTTAACTTGCAGTGGGAGCTTGAATT
TTCCATTTATTTTTGTGACCATTTAGTCTATAAGAGTCTCCGTCTTTACAGGGCCCCTCAC
[C,T]
TGACTACAGACTCCATAAAGGCAGAGATTCTATTTTTACTCTATTATTACTGTATTCCCA
GCACTAAGCACTAGGATTAATACATAGTAAGTGTTCAACAGATGTTTACTGGATGATTAG
ATTGGCATTTTAAGGTAGTCTGAGATCACGTTTTAGACAAGATACTTCAGTTTAGTCCAA
TCTTTATTATTTATTAGCTACTAAAGAGAAATTGATAATTACTCATGGAAAGGCAGTTT
TTGTTTTACAGTCAACTTTGACCACTTTGAAATTTTTGCGAGCCCATTGGGAAAGGCAGTTT

TACTAAAGAGAAATTGATAATTACTCATGATATTCTTCTTTTTTGTTTTACAGTCAACTT
TGACCACTTTGAAATTTTGCGAGCCATTGGGAAAGGCAGTTTTGGGAAGGTGAGAACAAA
TTGACATTATTACCACCAGCAGGGTTATGTAGCCCAGGGAACAGAGGGTCCAGAAATGT
TCACATTATTGAGTTGCTGGGACCACAAGGAAAGATAATTAAGTGAAAATGTTTTTGTAA
TGGATTTTTATAAAATTGTCACCACAGTTTAAGAAAAGCGTGTGACAGGCAGCTACATAA
[T, C]
GAACATATACTGTTGTCAGAATAATCTCATTAAACTCAAATCTGTTTACTCTCAGTAAAC
TTTAAGGCTTTTCTCTCTACCCTAAAGGAGATGAAGATTTCAGAATCATTTTCAGATTCT
ACCAGCTGTATGCCCAGTAATAGTTATCTTGTTTATGGAAGAGTTACTTATTTCATGTG
GGAAAGAAGTCATCCGATTTCTATTTTTTTTTCCAAGCACTTCTGTATTCAAACCCTGATTAC

40287 CAGTTTTGGGAAGGTGAGAACAAATTGAAATGATTAACCACCAGCAGGGTTATGTAGCCC AGGGAACAGAGGGTCCAGAAATGTTCACATTATTGAGTTGCTGGGACCACAAGGAAAAGAT AATTAAGTGAAAATGTTTTTGTAATGGATTTTTATAAAATTGTCACCACAGTTTAAGAAA AGCGTGTGACAGGCAGCTACATAATGAACATATACTGTTGTCAGAATAATCTCATTAAAC TCAAATCTGTTTACTCTCAGTAAACTTTAAGGCTTTTCTCTCTACCCTAAAGGAGATGAA [G,A]

TTGCTGGGACCACAAGGAAAGATAATTAAGTGAAAATGTTTTTGTAATGGATTTTTATAA
AATTGTCACCACAGTTTAAGAAAAGCGTGTGACAGGCAGCTACATAATGAACATATACTG
TTGTCAGAATAATCTCATTAAACTCAAATCTGTTTACTCTCAGTAAACTTTAAGGCTTTT
CTCTCTACCCTAAAGGAGATGAAGATTTCAGAATCATTTTCAGATTCTACCAGCTGTATG
CCCAGTAATAGTTATCTTGTTTATGGAAGAGTTACTTATTTTCATGTGGGAAAGAAGTCA
[T, C]
CCGATTTCTATTTGTTTCCTCATTTGTCTAATGTTTTTATCTTAAGAAAAAATACATATTC
AGTTTAATTTTTTTTGCAAGAAACTTCTGTATTCAAACCCTGATTACTAGTTTCTCAATG
GAGACGTACTTTAAGAGAAAATATTTCATATAAAACTTGCATTTTAAAATCATTTTCTG
TTTACTTTTTCAGGCATTATACAGACCTCTAAAGAAAATTTCAAAAACATGGACATCATAT
TTAGTGTTTTTCCAGTCCTTAAAGTCCTTTTTGGTTATATCATGTATTGGGTTGTAAACCAG

FIGURE 3QQQ

TTGATTCCCCAGGTGGCTTTTGTTAATTGAGATTAAACCTGTAGCTGCACACAACTCCTC
AGGGCCTCTATCTCTTTACTCATGTCTTTGTCCCTGTGGATAGAAGGGGTCCACATGTGG
TTTCAGGAAATTAGGACACCAGATCATCTGTTTTAACTGGAAAGAACTACCTGTACTGAG
AGTGTGACAAGGTCCTTTCAGACTCTGAACATAGCCCAATAAATGGTATCAACCTTAAAT
AACGAGATTCTGAAAATATGATTAAGTATCGAGTTTGCTGGAGCCCAGAGCTTGAGGATG
[C,G]
CCACCTGGGAGCACAGATTCACTTTGCCCAGAATGTACACTCCAATTAGCAGCAGTTATA
AGTGGGGTTTTAAGAAAAAAAGACAAGGCAGTTCCTAAGTTATTTACCAAAAATTTACAT
TAAAATAATGTAAGCTATTGATGGACTATGCATTATTCTTTATATCACAAAATTTACAGGAA
CACAAAGATAATGGGTGAGGCAGCTAGTCAGGAACAAAATGGCTTTAAAATACTGTCCTT
GAGCATGGGTTTGAGGCTGTGACTGACATCCCATACTCATGTTTCTCTAAACCTAATAAA

FIGURE 3RRR

TGTGGATGAACTTAAGCAGTTTTGGCTCCTTTTATGTTCAGGAACTTAGTCCTGCATTGC

53140 TCATGTTTCTCTAAACCTAATAAATTGTGCATATCTCATATAGCTCAGACTGCTCTGAGC TGAACTTAAGCAGTTTTGGCTCCTTTTATGTTCAGGAACTTAGTCCTGCATTGCTAGGAA GTCTTATTCCCAGATGGTCCTGTCCCACATTTGGGGGAAAGGAAAGGATGAGTCTTAGT [G,A]GGGATTTTAACACCATCAGAAGCAAAATTGGGATGGCATCGCAGGGTGCCACAAATGAGA CCTCACCCAAGTCACTAATTTATGTAGCTACTGTTGCTTGTGGGATCATCTCCAGGCTTC AGAATACCATGCAGTTAGTTTTCTCGGAATAAGTAAAACAATGAGCTATACATAGTAGAA AAAATATCTATTCCATTGGAAAGTCAACTAAAAACATCATGAAGAAAATTAAAATCCAGT 53848 AAGATAAATGTTATCAGGACCAACATACTTGTAAAATAAGCTTTAGTATTATATTTGGCC TAATTATTTGCATTAAGTGCAACAAAAATAATGAATGGCCATGTACGCATTTTTAAGTTG GCTTTGCTGGAACTTTTTCATAAGGAATCTCAGATTAGACTTTTAAAAGCCTCTCTAAAC TAGATATTGAAGCCAATAATTCACCATCAAACTGCCTGTAGCATCTACATAAATTGGGTG [A,T]ÄTTTCTCCCTTCTTCAGGTTCTGAAATATATTGAGGTTTCTAGGCCTGTCAAATGATGAC ATTCTTTACTTACTGCAAGGTCAAAAAACTTGTGAGGGTACCATGTAGACAAGGTATCAG GTCAGTTTTCCAAAAGGACTATTGATTTGGCTCTATAAAGTCAACTTCAATTCATCAAAG CAGTTTGGTCATATCTGAAAGTATGTCATTTCACCCAAAGCCTTGGTAAAATGACCAGCC TTAGTAAAATGACCAGTGTCTCCAACTGTGTACTGTTACAGAAGAAAACAGGTTCTTACT TATGTGAACTAAAAGGGATTTGAGTTATTTTCTATTTTTCTGATAAAATATTTAAGTGTT 57636 TCCTTTCTCTTTTGGCCAATTAGAACTCATTCATATATTTTTGTAATAAATTTTACATAC ACATGACACATATAAACATGCAGACACACACAGGCAGATTTTATAGCTTTGTAAGTTTCT TCATTTGCCAGTTTTCAATAGTTTCTCTCCCACCTTTAGACTGTCAAGCCCTAAACAATT GTTAGCTAGGCAACCTTAAATTTGTACTTCTAAAGGGATGACTCTTAGCTGAAACAAAGT [-,A]ÄAAAAAAATAAAAATTACACTTCAAAAACACAGAGCGGAGCTCAAACTAAGGGAGCAGGT GTATATAGGTAAAGGTCCAGTTAAGACAAGATGGCCAAGGAAAGCATCTTAAGTAAAGGT AGGACTTGTATAGATTTAAACCAATGTTAAATTTCTCATGACTCAGCTCTCCCTCTCCTC CAGGTGCACAGAGGCAGAAACCCTTACAAATGGAGATTTCCTTTATCAATGTAAATTTCA ATATAGCCAGCTAAATGCCAGCAAGGTATATTTTGGAGAACTGTTAGAGGCAGTGAATCT GTTTCCTTTCTCTTTTGGCCAATTAGAACTCATTCATATATTTTTGTAATAAATTTTACA 57693 TACACATGACACATATAAACATGCAGACACACACAGGCAGATTTTATAGCTTTGTAAGTT TCTTCATTTGCCAGTTTTCAATAGTTTCTCTCCCACCTTTAGACTGTCAAGCCCTAAACA ATTGTTAGCTAGGCAACCTTAAATTTGTACTTCTAAAGGGATGACTCTTAGCTGAAACAA **AGTAAAAAAAAATAAAAATTACACTTCAAAAACACAGAGCGGAGCTCAAACTAAGGGAGC** [A,T]GGTGTATATAGGTAAAGGTCCAGTTAAGACAAGATGGCCAAGGAAAGCATCTTAAGTAAA GGTAGGACTTGTATAGATTTAAACCAATGTTAAATTTCTCATGACTCAGCTCTCCCTCTC CTCCAGGTGCACAGAGGCAGAAACCCTTACAAATGGAGATTTCCTTTATCAATGTAAATT

GAAGTTATGTGCATGCTTACTTGAGGCATCTTTTTTTCCTTACCAGTTGACTGTTCCTAG
AGGAAGGTCATATACCAGTTAAACTCTACCATTTTTGCCTCTTAGTGTGCATGCTTGAGC
CTACTCGCCCACCTCCTGAGATCTTATCAGGAACCTACTGATCATCAGTTTCAGGGTTTT
TCTATCTACTGGGAGATTGCCTTTTCCTGGCGCCGGCTGCAACCAAATATTATTTGAGAG
AGACAGTTTAACAACCACCTGACCATCACTTACTAACACCAACCTACTTA

TCAATATAGCCAGCTAAATGCCAGCAAGGTATATTTTGGAGAACTGTTAGAGGCAGTGAA TCTGTATGTGTCTGCAGCAACTTCAATTCTTGCCTACTCTCAAAATAAAAAATTCAACTG

AGGTCATATACCAGTTAAACTCTACCATTTTTGCCTCTTAGTGTGCATGCTTGAGCCTAC 58649 TCGCCCACCTCCTGAGATCTTATCAGGAACCTACTGATCATCAGTTTTCAGGGTTTTTCTA AGTTTAACAACCACCTGACCATCACCTAATGGTTGTCTGACATTCCTTGGTGGAGGTTGG GGGTGATCTCCTGCCTTGCCCATGTCTGCCTGCCTACTGTAACAGACCAACTTAGTTAAA [T,C] TTTAATGAACAGGGCAAAGAAAGCCTTCTCTATGCCTGGACTCGGCATGGACAGCTCTGG GAAAGAAGAAAGCCTATTTTACCTGAGGGCCTATCTTTTATAAATATTTTGTTCAAATTC TTTCTTTTAAAACAAAGGTTCTTTTTCAATGACTTACCAAACCAATACACCTTAACCAAG GTTATGTCTAAACCAAGGATCAACTAGGCATTTCCAAAGAGTGGCAAAGTAGTCCTCACA GGTGGCCTTCAGAGCCACAGCATCAACAATATTAACTTCCCTATTAGTAGTGTTCTATTA 62188 CTTTGGGTTTTACATATATTATCTCATTTATTCATCATAACAACCTGGTTGATAGGGATT ATTATTCCCATTCTATTCCTGAAGAAACTGAGGCTCAAAGGAGCTAAAATATTTTCCTAT AGTCACACAGCTAGGAAGTGGCAGAGCGAGGACTCAAACCCAAGAATCCTGACTTCAAAG CCTCTGCTCTTCCTGCTGCACTATACCATCCCTATACACATCTCTGAGACTCCTGTAAAA [A,T]TATGTAAGGAACAGGATTTATTTCATTTATTGTCTTTCATATCCCACAAGAATACAAACT GTGTAAGGCAGGTATGTCTGTATGTTTTTTATCACTGCCTCATTCCCCCATCTTCCACAAC TGTGTTAGTGTTAGGGCTAAGGCCTTTGGCTTCTGGTTAATTGCCCTTTTTGCCATTATG CCAATGTCATTTGCACACTCACAAACATACCCTCATATAATCATATGCACTTCAGTTTCT CATCTCAAGATATGTCAAATAAGTGTATTTGGGGTGAAATATTTTTGGTTTCCTTTGCTA 63478 GAAATGAAATGTCCCTGCTTCCCCATAGCCAGAAAAGATTCTTGAGTGGACAACTGCACC TAAACTTGAACCTGAGCACTAGAAAGTCTTTTGTTTTATTCTATGTTTTTATAAATTTAA ATCTAATTTTTTGAATATAAAATAATACATATTTTGTAAATGTGGAAACACAGAAAGTTC TAATGAAAAAATAAAAACCTGTATTTCATCACGCAGAAATATCTGCTGTATTAGTTTTCC [G,A] TTGCTGCGGTAACAAATTGCCACAAACCTGGTGGCTTGAGACATCATAGATTTAGTATCT TACAATTCTGGAAGTCAGAAGTCCAAAATCAGTCTCCCTAGGCTAAAATCAATGTGTCAC CAGGGCTGTGTTTCTTCCAGAGCCTCCAGGTGAGAATCTGTTTCATTATCTTTTCTAGCT ATACTATCTTCAAACCTCTCTCGACTCTGACTTCATGTTCTCCTTATTCATCTTTTAAG AACCTTTTTCTTCTGCCATGAGACTAACCCTGGCTTCTTCACGTGCGGGTGGAAGGGTTC 65457 CTAACAGCAACAGCTGACAAACTTAATGAGCAAGCACTTTTTCAGCCTCTGCCACAGTCA CATTTTCTATCCTATTGGCTAAAGTAAATCACGAAGTCAGGCTCAGATTCAAGGGGTGTA GAAATAGGCTCCACTTCTGATGAGTGGCACGGCAAAGTCAACATTGCAAAAAGCCAGGCA GAGATATTACTGTGGCCAGTTTTGCAAACAATCCACCGTAATACATAAAATATGTTTAAG [C,A]AGTCCACAAAATGATCAAGGAAATGGTAGAAACTATAAACACTGCAAGAACTCAGAGCCA CATGATGTTATTGAGTCCTTGTAGTGCTCTGAAAGGGTTCAAGGAAGAAGTTGTTTTGGC ATATGACCCTGATGAACTTGCAAAAGTAGAGAAGAAGGGAGCACAGTTTCTGAAGAAGAA CTTAGTAGAGAAGTGTTATTCTGTGGCCAGTACGCAGTAATTGTTCCACCTAGAGATGTT GACTGACTGATGAACAGGAAGCTGAGTCTTTATAATGCAGATATTCACATATTCATTTAC CTGTAAATCCCAGCTACTTGGGAAGCTGAGGCATGAGAATCCCATGAATCCTAGAGGTGG 69947 AGGTTGCAGTGTGCCGAGATCATGGCGCCAATGCACTCCAGGTTGGGCGACAGATCCAGA CGCTGTCTCAAAAAAAAAAAAAAAAAAAAAAAATCTTTGCCTATGCCAACGTGGAGCTA TTCTATCCTGTTTCCTAGAAGCTTCACTGTTTTAGCTTTCACATTTAGATCTACAGTCTA GGATCAAGTTTTATTTTGTCTTCATATAAATAAGTAATTGACCCTTAGCCATTTGTTGAT [A,G] AGCTTATACTTTCCTTACGTCACCACAGAACCACATTTGTTATTAATCAAGTCACCATCT ATGTATGGGTTTCCTGACTCTGTTCCATTGATTCATTTGTATACTCTTGCATATTTATCA CTCTGTTTTAATTACTGTAGTTTTATACTGGATTTTCAGTAATTCATCTTTGGATTATGT TGGCTACAGTTGGTTCTTTAAAATTCCATATAAATTTCATAAGTAGCTTTTCAATTTGTA

# FIGURE 3TTT

69981

TTTTAAAGCTGCTGGTATGTATATTGGGTACATGGAGTCTATAGATTAATTCAGGGATAA
GAGAATCCCATGAATCCTAGAGGTGGAGGTTGCAGTGTGCCGAGATCATGGCGCCCAATGC

TTAGTAGAGAATTAGAATAGGATTITCTAAGTATCCATTTGAGACTTGTAGTTATAATTA
AACAAGAATCTATCCTGCAGATTTGTATTTTTCTCCTTAGATTGCACTTAATAGATCACCC

71903 TGCAGATTTGTATTTTTCTCCTTAGATTGCACTTAATAGATCACCAGGTTCATTTTTGTTG
CTGTTTAAAAGCATATTGAGTTTAAGCAGGATTGGAGTTTAATTGGGTGAGGTATTCTCA
CTGTGACTAAGTTTGATGAATTGAAAAGCGTAGTTGTAGAAAGGAAACTCAAGAAGGAAA
TTCTTGGGGAAACTTAAAGAATCGTATATATGCAATGTCACTTTTTAAGACAACTAATAT

71908 ATTTGTATTTTCTCCTTAGATTGCACTTAATAGATCACCAGTTCATTTTTGTTGCTGTT
TAAAAGCATATTGAGTTTAAGCAGGATTGGAGTTTAATTGGGTGAGGTATTCTCACTGTG
ACTAAGTTTGATGAATTGAAAAGCGTAGTTGTAGAAAGGAAACTCAAGAAGGAAATTCTT
GGGGAAACTTAAAGAATCGTATATATGCAATGTCACTTTTTAAGACAACTAATATTTTTA
AGAATTTACTACTTTTGAGGTGCTGTACTAATATTACATGTATAATTTCATATATCTT
[C,T]

TGCTGATGATGACACGTTCCATTTCTTTCGATAGCCACAAAACAGGAAGTGATGACAAA
[G,A]
CTGGATTCTAACTCCTGACTCCCAAATTCTCTAAGACCCTCAGCATTAACATATTTTA
TTTTAATGTTATTATATATGTATCATTACTTTTACAACTCTTAAACCAAACCATTTTAAAA
TTAGCTACAACTGCAAAATCAACTTAAAAATTTCAAAGAGCCATTTAACATGATAAATTA
AAATATTTTAGTAAAACAAAATCACCACTGATACTTTAATATTCTTAGGTCTGAGAAAAC
CCATTATGTCGTATTATTCCTGCGTTCCTGGTAGCGTACTTCTACAAACCAAA

TGAGGTATTCTCACTGTGACTAAGTTTGATGAATTGAAAAGCGTAGTTGTAGAAAAGGAAA
CTCAAGAAGGAAATTCTTGGGGAAACTTAAAGAATCGTATATATGCAATGTCACTTTTTA
AGACAACTAATATTTTTAAGAATTTACTACTTTTGAGGTGCTGTACTAATATATTACATG
TATAATTTCATATATCTTCAACTACTAGTTCCTGTAAATAAGTATGCTGATGATGACACG
TTCCATTTCTTTCGATAGCCACAAAAACAGGAAGTGATGACAAAGCTGGATTCTAACTCC
[T,C]
GACTCCCAAATTCTCTAAGACCCTCAGCATTAACATATTTTATTTTAATGTTATTATA
TATGTATCATTACTTTTACAACTCTTAAACCAAACATTTTAAAATTAGCTACAACTGCAA
AATCAACTTAAAAATTTCAAAGAGCCATTTAACATGATAAATTAAAATATTTTAGTAAAA
CAAAATCACCACTGATACTTTAATATTCTTAGGTCTGAGAAAAACCATTATGTCGTATTA
TTCCTGCGTTCCTGGTAGCGTTTCTACTGCTGGACATCAGAAATAGAGAAATAGTAGAGACC

TCTGTAGAAAATAATAGCAAAATTTCTCCCTTGAGAAGCTTCATAAATTAAATCTCC
AGAGCCAGTATATGTAAGCCGACAGATTATGAAATATGATTTAATGCTCTGTCCAGAGAA
AGGTCAGGGCTTCAGAAAAATCATCATAATATCAAGAAAAACTAATCTGCAACCTGTTAT
ATGATTTTAAAAATCACCCCCCATCTTTTTTACTGTGCAAACTGTAGATTTTTGTTTAT
TTTATTTGAGGCTATAGTTTATGTCTTGAATCACACACATATGAGTATTACTTTCTGTGA
[A,G]
GTTTTCATGACCCCTGCAATCAAACTTGGGTCCTTCTGTTAGTTTCTATCACAGTATCCT
TCACTTTTCTTTCACAATTCTTGCCATATTCTATAACTACATATTTGTTTAAATATT
TGTTTATCTTTTATAGATGATTGGCTTCAGGAAGAGGGAAACCATGTCCTTTTGTTCAGT
CCTTTATTCTCAGCACCTTGCACAACATGAATATACAAAAAAATATTTGTAAAAATGACCAT
CGAATGAACAAGTGCTCATTAAGTACCAAGCTATATGCCAGGGGTTGCTGATGGTTAGAA

74121 CTCTCACCTCAACCTCTTAAGTAGCTGGGACTACAGGTGCATGCCACTATACTGGCTAAT
TTAAAAACAGAAGCCAACAAACAAAAAACACACCTTTTTAAGACTGGGTCTCACTATGTT
GCCCAGGCTGGCCTTGAACTCCTGGCCTCAAGCGATCATCCTGCCTTCCAAAGTGCTACC
TTCTAGAGTATTGGGATTACAAGCGTGAGTCATCTGCACCAGGCCTGAAGCATTCTGTAA
TGGAGAAATACCTGGGTGCTATGGAAGGGCAGAGGGGGAAACACAGAGGAGTAACATCTA
[G,A]

FIGURE 3VVV

TTTACGTTTGTCAAGGAGAGGCCAGGAAAGACTAACTACAGGGGAGATAAACTCCAACCA AGAGTCTTTAAGTCTTCCAAGACTTACGTACAAGTTTCTTATTGCTAAAATGGAAGTTTT AATGAACATTTATTTATTTGAGATGGGGTTTCACTCTTGTTGCCCAGGCTGGTGTG CAATGGCACAATCTTGGCTTACTGCAACCTCTGCCCCCCAGGTTCAGGTGATTATCCTGC CTCAGCCTCCAAAGTAGCTGGAATACAGGAGCCTGCCACCATGCCCAGCTAATTTTTTT

CACTCCAGCCTGTGCTACAGAGAGAGACTCCGTCTTAAAAAACAAAACAAAATAACAACA 75646 ACAACAAACAAAGATAGATGCATAGAGTTTTTCACTGTTGCACTATTTATATTAGCCAAA AACCGGGAAACAACCTGAATATTCATCAAGTGGGGACAGGTTGAGTAATCATGTGACATA CATAAATTGCAGCACTGCACACTTGAGAAAAGAAGTGAGAAATGTCTCTATTTCCTAGTG TGGTTTGCTCTCCAGAGTATACTGTTAAGTGAAAAAAGCACTGTGGCCTCAAATTTATCT [A,G] TAGATTCTATACAATCCCCATCAAAATCTCAGCTGGCTTCTTTGCAGAAATTCACAAGCT GATCTTAAAATGTGTATAGAAATCCAAGGGACTCAAAATTCAATAAATTCAAAGACTAGC CAAAACAATCTTGAAAAAGAAGAGCAAAGTTGGAGGGCTCATACTTTTCAGTTTCGAAAG TTGTTATGAAGCTACAATAATCAAGATAGGGTGGTCCTGGCATAAGGATAAACATGGAAC

TAACAACAACAACAAACAAAGATAGATGCATAGAGTTTTTCACTGTTGCACTATTTATAT 75698 TAGCCAAAAACCGGGAAACAACCTGAATATTCATCAAGTGGGGACAGGTTGAGTAATCAT GTGACATACATAAATTGCAGCACTGCACACTTGAGAAAAGAAGTGAGAAATGTCTCTATT TCCTAGTGTGGTTTGCTCTCCAGAGTATACTGTTAAGTGAAAAAAGCACTGTGGCCTCAA ATTTATCTATAGATTCTATACAATCCCCATCAAAATCTCAGCTGGCTTCTTTGCAGAAAT [C,T]

CACAAGCTGATCTTAAAATGTGTATAGAAATCCAAGGGACTCAAAATTCAATAAATTCAA AGACTAGCCAAAACAATCTTGAAAAAGAAGAGCAAAGTTGGAGGGCTCATACTTTTCAGT TTCGAAAGTTGTTATGAAGCTACAATAATCAAGATAGGGTGGTCCTGGCATAAGGATAAA CATGGAACAGAATTGAGCATCTAAAAATAAAGCCTCATATTTCCAGTCAATTGACTTTTA ACCAGGGTGCCAAGAAATTCAATGGGGGAAGAATTTGTCTTTTCAACAACTGGTGCTGG

AGAATTGAGCATCTAAAAATAAAGCCTCATATTTCCAGTCAATTGACTTTTAACCAGGGT

79007 TGAAAAGTGGTAAATAAAGGAAAGACTTCAGTTCAAGACCAGTCTGAGCAACATAGTAAG ACCCCATCTCTACAAAAATTAAAATATCAGCTGAGCATTGTGGTGTACATCTTTAGTCC TAGCCACTTGAAGGCTGAGGCTGGAGGATTGCCTGAGCCCAGGAGTTCAAGGCTGCAGTG AACTATGATGGCACCACTGTGGTCCAGCCAGGGTTAAATAGCAAGACCCTGTTTCTGGCG [-,A]

ĀAÁAĀAAAAAAAAAAAAAAAGGAAGACTTAAACATACCTTTCCTATATGAACTGTGCCT CGGAGTAACTAAATAATTGATTAAAGCAAGTTTCTCTGTATAAAAGTACTCCAGCTAAAA CATTAAGGAGAAATGATAGAATTCAAATATCACAACCCCTAAGGAATTTTTGCATCAAGA CAACAATAATTAATGACTGATAACACCACACACAGAATACAGACTTATTAATTGTATAAC 

ATTGCAGGCGTGAGCCACTGCACCCAGCCCACCCTTGGTTTTTTTCAACAAAAATTACT 80043 ATCAATGGCAGTGGGCGGCTTTGTTTGAATCCAACTCTAGCATGCAAACATTTGATAAA AATTTCTTTATTTAAAAAGAAAAGTTTACAAAACAATCAGAAAAAAATAAAAAAGATTGAG GATCTCAGGACAACTACTAGCCTAGATAATTTATAAAGATTAGATAACTGACTCATTTTT [A,G]

TTAGTTTCTTTCCTAATAAGGCAATATGTATTAGATATATCAGAGTAGAAGGAAATATTT TTCTTACATCTATTTGGCTTTTTAAATATAAACATATATAAGTAAAAAACCAAAATGATTT TTGTGTGCTTTTTTCCTTTTGTGTTTGTGTGTTTATATCCTTTTTAAATATATCCTTTT TATGTACCTAAGCAGCTGTATACTATACTGCATACTATAGTGTGAACTTTGTTCTTTTCC

AAAAAAATTATGCAAATACTAGCATTTGTGTGCTTTTTTTCCTTTTGTGTTTTGTGTGTTTT 80499 ATATCCTTTTTAAATATATCCTTTTTATGTACCTAAGCAGCTGTATACTATACTGCATAC TATAGTGTGAACTTTGTTCTTTTCCTTCGTCTTTACAACATATTGTGGAAAACGTTCCAT TCTGTCTCATTTTTAAAAATGCTGTATAATCTGTAGCACGAATTTACTATAATTTATTC [G,C]

CATGCTCCCTTATCGATGGGCATGTAAATTGTGTTAATTTTATATGATATAATGAGTATC CTTATATGTATATCTTGGCACAGTTTTTCGAGTGTATCCATAAAGTTTCTTGCAATGAAA

FIGURE 3WWW

TGTCAGGTGTTTAACTTTGTGCATTTCCTCGTGTGAATGGGAGCGTAGGTCCAGCATCGT

CTTCTGGTGTCAAAAACTATTCAGGTGCATTTCTGTAACCTCTATGCACCTCTCCCCCCA 88843 CCTCCCAGGTGTTATATTTTACAGGCTGTCATACCCTTTTGTACCTCTCCTGAGGAGTTG TGACATTTGGTGTATAATTAATTCATTTGTCTCCTTTATAAAATTGTGAACTCTGCATGT GACCAGAAGTTCAGGCTTACAAGTAGGAAATATTCAAATATAGGACATTAAATCCAAAGG [C,T]ATACTCTGAGAGCTAAAGAGGATGCTATTAATATTAATAGCACTGGGAAGAGTCAAAAGC CATAAATAATCTAGGCAATTCAGGACCTATGTCAACATCATTAAGGCTTTTCAAGGCAGT GTTTTTTGTTTTTTTTTTTGTAGAGACAGGGTCTCCCTATGTTGCCTAGGCTGGCCT TGAACTCCTGGGCTCAAGCAATCCTCCTGCCTCAGCCTCCCAAAACTCTGGGATTACAGG ATACTGTAATTCTTTTTTAAACCTCCTTCTTCAAAAGAATCAGCCCGATTCATGTTGTAC 89700 TTGAATTCAAGATAACAAAACACCTTTTAGTTACTTAGAAAGATTAGATTGTAAAATATG TGCTGAGTTCCTAGAAATTAAAAGTGAGAATGAAAAAAAGAATCAATGAAAGTACAGTAG ATCTCCCGGACAAGGAGACCATCTGCATAAAACTGAAGATATAAAATATGTGACTTCC TACTTTTAGATTAAAATCTACATTTTGCCTTTGGACATGGTAGAAGATTCAAAATTACCC [G,A]TAAACAGTCAGCACTACGTGGAAGTAGGAGCAGCAGTAGGCTGCTGTTTGCTTAGGGTTT CCTGGGTACCAGGCTGCCTAAGCACTTGTGAGTTATTTCACTCAGTCTTCCCATAGC TCCAGGAGGTTTATGGCACTTTGTCCCCATTTCACCTTCGATGAAACTCTGGTTCTGAAA

AATTACTTGCCCAAGTTTGCATGGCTATTAAGTAGGGAAAGCATCATGTTTAGGAAATGC AGAGCTCTTCACCACTCTCCAGCCTGCAGATGCTCAGCATGGCTGCAGCTCTGAGGGGAG

FIGURE 3YYY

TCCTCTAAAGAAGTTGCACTGCATCACAGTTCCATACCAATTTCTGCTATGACCTTAAAT
ATAGCCCTGAACTTCCCTGTCAAGGAAGAAGTGAGGAGGTTTCAACAAGTGATCAGTAAT

GACAGGTGTCTGGGCACAGTCTAGTTGAGTTCTCGGCACAGCTGCCATTAAGATGTCAGC 92558 CAGAACTGGGTTCTCTTCTGGAGGCTGAACTGGGCAAGAATCCACTTCCAAGCTCAGTCA ACTTGAATGATGATATATAACATTGTAACATAACTCAGTCACAGAAGTAAGACCATCACA [T,C] CTGCCATGTAATGTCGGTTAGAAACAAACCATGGAACCAGCCCATGCTGAGGGGCTGGAA ATTATGCAAGGGTGTGAACACCAAAAGCTGGGAATCCTGGGGGTCACCGTACACAGTCTG TTCACATTTCCTCTAAAGAAGTTGCACTGCATCACAGTTCCATACCAATTTCTGCTATGA CCTTAAATATAGCCCTGAACTTCCCTGTCAAGGAAGAAGTGAGGAGGTTTCAACAAGTGA TCAGTAATGATTCTTTTATGTCTAAGATTCTAGGATGATTTCCTCTCTGCCCTGGTAGGC AAGCTCAGTCAGAATGTTGGCAGGAGGTATTTCCTTGTGGCTGTAGGACCCATGGTGGCT 92667 AGAGTACACATACTTGAATGATGATATATAACATTGTAACATAACTCAGTCACAGAAGTA GAGGGGCTGGAAATTATGCAAGGGTGTGAACACCAAAAGCTGGGAATCCTGGGGGTCACC [G,A] TACACAGTCTGTTCACATTTCCTCTAAAGAAGTTGCACTGCATCACAGTTCCATACCAAT TTCTGCTATGACCTTAAATATAGCCCTGAACTTCCCTGTCAAGGAAGAAGTGAGGAGGTT TCAACAAGTGATCAGTAATGATTCTTTTATGTCTAAGATTCTAGGATGATTTCCTCTCTG CCCTGGTAGGCTGCTCTTCAAAGTATGACCTCCTCATTGTTTCTCTGCTCTACCACACAC TCATTCCCCTCCAAGAAGGCTGCCCACCTGTAATGACCTGTCTACAGAGCCTGTGATAGT 92803 CATGTAATGTCGGTTAGAAACAAACCATGGAACCAGCCCATGCTGAGGGGCTGGAAATTA TGCAAGGGTGTGAACACCAAAAGCTGGGAATCCTGGGGGTCACCGTACACAGTCTGTTCA CATTTCCTCTAAAGAAGTTGCACTGCATCACAGTTCCATACCAATTTCTGCTATGACCTT AAATATAGCCCTGAACTTCCCTGTCAAGGAAGAAGTGAGGAGGTTTCAACAAGTGATCAG [A,T]ĀAŤGĀTTCTTTTATGTCTAAGATTCTAGGATGATTTCCTCTCTGCCCTGGTAGGCTGCTC TTCAAAGTATGACCTCCTCATTGTTTCTCTGCTCTACCACACACTCATTCCCCTCCAAGA AGGCTGCCCACCTGTAATGACCTGTCTACAGAGCCTGTGATAGTGACTTGTGATAAATGG CTATTAGCACATTTACCAATCAAGGTCCTGTTTGCAATTCGGTTGTGGGTCAAAATTATG TTTGTTTTAACTGAGGTCTTTAGTTTATTTCAGGCAGAGATCTGGGCTGGAGTGTCACCT TTTGGTAAATCTTCTTTTCAGTAGACCACAAGCCCTTGCAAATGTTCTCTTTTTCTAACT 95079 CTGGTAGCAGAAGGACCACTTGAGCCTCAAAACAAACGGCAGTGCAGTAATGAGGGTAT ATTACACATTGTGAAAACAGGAGAATCTGCCTTCTTTGTGTTGTATGCATCAAGCAGTTT CAAAAGGGCTTTGCAATTGTGTTTCTCACACAAAGCCACCCATTTGTGAAAACCCATGTG [T,A]AAAGGCAAAGAGAACTGTCTGTGTACAGGTTAACATTTAACTAGACTGGCAGAGCTTTTA ATAATTTCTATAAGGTTAATGGCTTCGTTAATATGCAACCTGTGATTTGGTCCAAGTTAA ATTITACTTTGCCCAGAATACATTATAATATAAAGCTTAAGCTTTATTCTTTCAGGTTTA GTCATTTAACACATAATATTGATCAATTATGCATGTTGGACACAGAGCTCTGAATAGAGC TTTGAAATATAAAACTATGGTTTTAGTCCTCTTAGAGCTATGATGTTTGGTAGGTTAGGT CTTCTTTCAGTAGACCACAAGCCCTTGCAAATGTTCTCTTTTTCTAACTCTGGTAGCAG 95089 GTGAAAACAGGAGAATCTGCCTTCTTTGTGTTGTATGCATCAAGCAGTTTCAAAAGGGCT TTGCAATTGTGTTTCTCACACAAAGCCACCCATTTGTGAAAACCCATGTGTAAAGGCAAA [G,A]AGAACTGTCTGTGTACAGGTTAACATTTAACTAGACTGGCAGAGCTTTTAATAATTTCTA TAAGGTTAATGGCTTCGTTAATATGCAACCTGTGATTTGGTCCAAGTTAAATTTTACTTT GCCCAGAATACATTATAATATAAAGCTTAAGCTTTATTCTTTCAGGTTTAGTCATTTAAC ACATAATATTGATCAATTATGCATGTTGGACACAGAGCTCTGAATAGAGCTTTGAAATAT AAAACTATGGTTTTAGTCCTCTTAGAGCTATGATGTTTGGTAGGTTAGGTGAAGTAGACA GGAAGCCACACTGCGATTTTCCAGATAATTGTGAAACAACTACGGGCCATTACAAAACCA

TAGGAAATTAGAAGTGAGGAGTAATTTGGAGACTGACAAGCTCTACCTTCATCTAAAGGC

AGAATTTCTTCTGCAGTCTCCCTAACAAGGAATCGTTATACCTCAGGGATGGGATAGTCA CTACCACATAAAGTAGTTCATTTTCAGACATGCATAACCTTAGAAAGTTCTTCTCTTGAT TTACAATTAGCCTCATAGTTCTGTTGCTGCCTATTGGAGTTTTACTACGTGTACAGTCAG

97070 ATAGTGTGGAATAAAGTATAAAAAGGGCTTAGCCTGGTTTCTCAAATATTGCAATAAATG
AAACTTAGCATCATGATGCTGTCACAATGGTTCAATGATAATTGAAAACATCGATTCATC
ATTTAGCATCCTCAGCTTATCAGTTTCTCACTATCTAGCTCTTCTTACACTGGACACTTC
CTAATTATTCTTTCAATGTTTTCTGGAAGTTAGTTGAATAATTACTGTGCACCAGATACT
ACACAGTAGTCCCCCTTGATGCATGAGGGATACATTCAAGACCCCCAGTGGATACCTATGGT

[T,A]

TTAGATGAGACATTGGACTGTGGACTTTTGAGTTATTGCTGAAATGAGTTAAGACTTTGG
GGAATTCCCAGAACTGAGGGTTCCTCCCCATTGTAGACCATATAGGTAGCTTCCAGACGT
TGCCAAGGCATTTGTAAACTGTCATGGTGCTAGTGAGAGTGTCTTTTAGCATGCTCATGT
ATTATAATTAGTGTATAAATGAGCAGTGAGGATGACCAGAGATCACTTTTGTCACCATCTT
GGTTTTGGCCAAAAACAGTCCTGCTGATTACTAAATTCCTATCTCACCTATTCAAGATGGAGTCA

CTTGCAAAAACAGTCCTGCTGATTACTAAATTCCTATCTCACCTATTCAAGATGGAGTCA CTCTGGTCTGAATGCCCCTGATAAGAGAATCCACAGTGTTCAATTCTCCCCAGTTGATTC TGAAGCATATCCAGGTTTATTAGCCACTAAGTAAAAATATATTATAGACTACTGTCAATG AAAGAAACATTTTGTAAGTTATTTCATATTTATTTTTACTTGAGAAGACTGAAAAGGTAA AGAAGTGATGCTAAAATTTAGAACTAGAAAATCTCAACTTGCTCTAGTAGGAATTTTAAT

AGTITCTTTCATTTCTCTCTCCTGGTATGTGAATAAACAACCTTCCATACTGCAATTT ACCCTGTAGTGAATTAGATGTTACCCTATTATATTTTGGAGAAACTATATAGTTAGAATC TAAGCTTAGATAACTTATTTTTATGTTTACAAATCCACTTTCTCTTATACATTTTTCTTA AATTTTTCTCATATTCTTCTCTGAATTTGTGGTAAAAATACCCCTTTCCCATTCTATGT CATGGTTCTTTACGAAGCTTTCTCATCTCTCATCCCATCCCGAGGGAACTATGTCTCATTTAT

FIGURE 3AAAA

TAAAATTTAGAACTAGAAAATCTCAACTTGCTCTAGTAGGAATTTTAATAGAGCACACTA [A,C] GTTTCTTTCATTTTCTCTCCTGGTATGTGAATAAACAACCTTCCATACTGCAATTTA CCCTGTAGTGAATTAGATGTTACCCTATTATATTTTGGAGAAACTATATAGTTAGAATCT AAGCTTAGATAACTTATTTTTATGTTTACAAATCCACTTTCTCTTATACATTTTTCTTAA ATTITCTCATATTCTTTCTCTGAATTTGTGGTAAAAATACCCCTTTCCCATTCTATGTC ATGGTTCTTTACGAAGCTTTCTCATCCTCTCCATCCCGAGGGAACTATGTCTCATTTATC CTAGAAAATCTCAACTTGCTCTAGTAGGAATTTTAATAGAGCACACTAAGTTTCTTTTCA 102939 TTTTCTCTCCCTGGTATGTGAATAAACAACCTTCCATACTGCAATTTACCCTGTAGTGA ATTAGATGTTACCCTATTATATTTTGGAGAAACTATATAGTTAGAATCTAAGCTTAGATA ACTTATTTTTATGTTTACAAATCCACTTTCTCTTATACATTTTTCTTAAATTTTTCTCAT ATTCTTTCTCTGAATTTGTGGTAAAAATACCCCTTTCCCATTCTATGTCATGGTTCTTTA [C,T]GAAGCTTTCTCATCCTCTCCATCCCGAGGGAACTATGTCTCATTTATCTTTAGGTTTTCT GTATCTTACTACAGTGACTTACCAGAGTAGGTAAATATCTGATGAATAAATGAATACAAG ATTTAATTAAGAAGTAATCACATTAAACTAATTGTTCCCTCTCTGATCTCTGTAATATTA AGAAAAATGGTGCTCAGGGATTTAACAGAAAGCTCATAAAATGTCAAATCCACAGCAATT GTTTTATGCGGCTTTGTCTATGCTGGCACATAACTAGTATGTACCAATGTATCTCAGAAA 106162 AGATATCAAGTTTTCTGTTTAAAAATTTCAGTTTGAGAAAAATCAGTTAAAGAAAAACAT AAAAAAGATAAAAGTATATGTGTTATCTAGATTTGTGATATAGGGATATGGCAATAATCA AGATGGTGATAAGTGAATGCTGAATTTCAAGAACTACTGATTACACCCTCTAGAATAAGC [G,T]GGATTTATTAGAATATCAGGGAAGATCTGCAGGGCACAAAAACTGTATGTTATAAATGTT AACAGTGTCAATAAGATCTTTGTTATGTCTTTAGAAGGCTGCTAGATGAGGAGAGTCCTA GATCTTAAAGGCTCCTTATTCAATTTTTACAAAAAGGATTTGCAAGTGGAACTGAAACTC CAAGTACCATCTATTGCTCATTATTTATTTACCTATTTTTGAGCCTGATTTTCCTGATCC CACCTGTGCTCAGGGGGCTAAGAAACACTGGTAATGACCTCTAATTTCAAAGCTCACTGT CTGATTACACCCTCTAGAATAAGCTTTTGCCCGTGATGATTAAATGTGTACGATTTCTTC 106378 CTAATATTTATTTTTGTGTATATTGGGATTTATTAGAATATCAGGGAAGATCTGCAGGGC ACAAAAACTGTATGTTATAAATGTTAACAGTGTCAATAAGATCTTTGTTATGTCTTTAGA AGGCTGCTAGATGAGGAGGCCCTAGATCTTAAAGGCTCCTTATTCAATTTTTACAAAAA TTTTGAGCCTGATTTTCCTGATCCCACCTGTGCTCAGGGGGCTAAGAAACACTGGTAATG ACCTCTAATTTCAAAGCTCACTGTCATTACTTATTTATGGACTGTCCAAAAAGATTTTTT CCACTTTCTTCCAATGCCTTATTTCTTCCTTACCTTTACTGCTTCTGACATTTGAAAACA GGGTCTCTGATTCTCAGAAATGTGAGCAATGGTGAGATTTAGCATGAAGGTGACTTTCTT AGCTTTATCCTCCCTTCAGAGAACAGTGTTTTCATCCCAGGTCTCATCCATGGCTTCACC 107310 CTACTTCTATCATTAAGGCATCCTATTCTCCTTCAGTCAACTTCTTCCTCCTCCTCATTT TCTTGGTGACTTGGTCATTGCAGATGAGGAAAAACATGAAGAAATCAATTAATCTTCAAG TTTAACCACCTTTAGAGACTACCCTTGTGAAAGATTAATTGTGTAACAGTGTGGTTAAGA <u>ATGTGACTTCTGGAGCCAGATTGCCTTCATTCAAAACACACTTCACTCATTTCCTAGCCC</u> [C,T]

GAGAGCTTTGACAAGTTGCCTAAACTTTGTCTTAGTTTTTCCAGGGATCAAAAGAATACT
TACTTAGAAAAAAAATCTTACTTACAAAAGAAATCTTACAGGGATCAAAAGAATACTTAA
TTAGGGTCATTGTAAAGACTGACCTGATACGTGTGAAGTACTTGATGCAATGACTGTCAC
AAAGAAATCACTCAATAAAAAGTCTAATATTAGTACAATTCTTCTGAGGCAGTCATGGCTT
TCTTTCCTTGGAAAGGAAGCTGGGACTGCTTCATCTTGTTTTATGTTTCTTTGTCTATGC

108663 ACTITCCATGTGGAGCTCATATTTGAAGACCTCATTTGCCTTCTCCATCTCCATTTATAA TATTTCATCCCTGATGGGCTGTCGCTTGGGCCTCATGTGGAAATTGTAGCCACCTGTGAAG GGTAACCACCTATCTCTCTGGTGCCCCCTATGCGCATCCCTACAAGTGAGCTGTATCA CACCATGCTGCTTACATTTTTATGCAACACGATTCAGTAACAGGCAGAAACTTTTATTCT TACTGACTCATATTCTTTATATTCATCTGAAAAGATTGACATTTAAAGGAGCCAATTGTA [C,A]

FIGURE 3BBBB

AATGGGAAATCCACTGTGTGAATATTTCTTGTACATCAGAATTTGCCTTAAAAATGTTTT
TAACTTAGAGCACATCTGTACTGTTCTCCCCAAATGTCCCATTTACTAGTTCAGAGCAAG
ATGACATTAGGTCTTGGGTGACTCCTGACCCACTATCCTAATGTATATTTTCATTTCCTA
CCAATGTAAGTACCCCATCCAATTCTATCAATACCATAGTGTCTAAAATTCTTGTATTTT
TCTTATTCAGGAAATGCTACAACCAGAGGAACAGTAATGTCTGCCTGACATATCAGAGAA

TCAGTAACAGGCAGAAACTTTTATTCTTACTGACTCATATTCTTTATATTCATCTGAAAA
GATTGACATTTAAAGGAGCCAATTGTACAATGGGAAATCCACTGTGTGAATATTTCTTGT
ACATCAGAATTTGCCTTAAAAATGTTTTTAACTTAGAGCACATCTGTACTGTTCTCCCCA
AATGTCCCATTTACTAGTTCAGAGCAAGATGACATTAGGTCTTGGGTGACTCCTGACCCA
CTATCCTAATGTATATTTTCATTTCCTACCAATGTAAGTACCCCATCCAATTCTATCAAT
[A,T]
CCATAGTGTCTAAAATTCTTGTATTTTTCTTATTCAGGAAATGCTACAACCAGAGGAACA
GTAATGTCTGCCTGACATATCAGAGAAAATGACAATTATGTCATCATCTGTCACTTAGGT
TTCTTAATACCATCCTGTTACAAGGAATAGAGGCAAAAACTCAGCGTAGGAGGTGAGAAA
AAACTGAGGCTGCCATCTTAACAGCCTTTTCATTGCAGAGTCTCAAAATGTACCAAAAGA
TGAAGTGGACAGTGTCCTTTTAAAACAACATACAGTGTAGAATACAGTAACTTATCCCCA

- 110733 CAACTGACGTGTAATGAGTACTCACCAGAGTTGAGATGTTCTGCTAAGCCAGGCCCTCTT
  TTAAAAATGTAATCTCAAACTTTATTAGGTCTCATAATCACCTGGAAGGCTTATTTAAAT
  ATTGGCGCCCAACCCACAGAGTTTCTGATTTGTTATAATAGAGTTGAGGGGGGACGGGGC
  GTAAGAATCTGCATATCTAACAAGTTCCCAGGTGATGCTGATGCTGCTGATCTGGGCACT
  ACATTGTAGGAATCAATTGGCTCTAAAACCTTCTCTACCTTCCACTTCTACATGAGCATA
  [C,G]
  ATAATCTTGTAGCTGAGTCAGCTTGGAAATCTATGCAGACTAAAGTAGACAGTTGCATGT
  CTGGCTGCTCATCTGAATCACCTGTGGAATTTGTTTTTTAATACAGATACCTGGCTCT
  CCTACAAGTCCCACTGAATTGGAGTTTCAGGAGACCGAAGCCCAGGCACATGTATTTTGC
  AAAACTACACTGAAGTTTCTGATAATGACGGATATCAACAATTAAACGCTTACTTCTTGC
  CAAATGCTGTGCTAAGTCTCCTGTAATCATCTTTCATTTAATATTTCTAATAACCCTCTT

AGAAAAAGAAAAACAGAGACAACCTACGCTATGATAAAGTTATTGAAATCAGGCATTGG

111546

FIGURE 3CCCC

TATTAACATATAATTAATGTAGTATATTGTATATATAGTACTATTGTTATAGTATATATTGTTCTCACTTCAGAAATTAGCAGACTGAAAGGTTAAGAAACTTGTTGACTGTGAAGCTGGAAGCAGACAGTCATAGGGGGTCTGATGCCAGAGCCCTAACTCTTAACATGCTGCAGTACTGTCCC

125444

CTTTGAGTTGTTTGCCCTCTAGATCTACACAGGCATGGGAGCAATCACTCTCATGG CTGGGGATGGGAGAGGGGACTTGCTTAAGTGGCTCTCTACAAAGGCACTACCCACATGG CTCTCTGTGAAGGCTCTGTCTACACAGCTCTGTTGAGTGGTGGTCCTGCCCTTCGAAACA GAGGTGGAGGCAACCCTGCTCCCCAAGCCAGTGCACTCTGGACCTGTAGTGGGAATGGCA GCCCTGATGATCTGTGAATCGCCCTCATGATCCTTCTTCCTTTTACTTGAAGGATAGCAC

GATGGGAGAGGGACTTGCTTAAGTGGCTCTCTACAAAGGCACTACCCACATGGCTCTC
TGTGAAGGCTCTGTCTACACAGCTCTGTTGAGTGGTCCTGCCCTTCGAAACAGAGGT
GGAGGCAACCCTGCTCCCCCAAGCCAGTGCACTCTGGACCTGTAGTGGGAATGGCAGCCCT
GATGATCTGTGAATCGCCCTCATGATCCTTCTTCCTTTTACTTGAAGGATAGCACATGTT
CACAGCTGGATAGCATTACGGTCCCAGCCTGTAAAATCCAAGAAGTCTGACAGCCTTTCT
[T,C]

[T,C]
GCAGTGGCTCATGCCTATAATCCCAGCACTTTAGAAGGCTGAGGCGGGCAGATCACCTGA
GGTCAGTAATTCGAGTCCAACCTGATCAACATGGAGAAACCCCATCTGTACTAAAAATAC
AAAATTAGCCGGGCATGGTGGTGGATGCCTGTAATCCCAGCTACTCAGGAGGCTGAGGCA
GGAGAATCACTTGAACCTGGGAGGTAGATGTTGCAGTGAGCTGAGAACACAACATTGTAC

FIGURE 3DDDD

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127506 CATTCTTTCTGCTGCTGTCAATAGCCCTCTTCTTTGGTCCCACAACACACCATCATGATT TCTGCATTAAAAATGCCATCTCCCAAGTAATTAACCTATTCACAGTAAGAACAGTTGTTA GAAGTTGGGGTTATTTCATCATGGTCCAATGGCTTTATCTTGCTCAGGAAATCAAAGATG [G,A] GAAGTCATTGTAGCACTATTTCTTAAGTATATTCAAATTTGGATAAGTTAGTCAAATTGA TGTGAAAGGACCACCCTTGTAAGCCAAATGTGTAAGTCCTACATAGGGATATTACCTGTT AGAAACATATCTGCTCTTTCCCACTTCACCCTTAATTTTTTCTCCCCAGCCAATTTACT 127878 CACCCTTGTAAGCCAAATGTGTAAGTCCTACATAGGGATATTACCTGTTTTTATCTCCTG ATGGGCTTTTTTTTTCAAGTTTCTAAATAAATCCAGTGAACAAGTAGATACGCTACTC TGCTCTTTCCCACTTCACCCTTAATTTTTTTCTCCCCAGCCAATTTACTCACCTTCTGTG GCTGTGCTTCTGTGTTAGACCCTTGCTAGCTGCTTCTGGGGTTCAGAGCAATTGTGCTCT [G,T]CCCTCATCTTTTATGACACACCTAGCAAAACAGAAGCAGAGGAGCGAGTTGAAACAGACA AACGACTATCTGTTATTCTTCAAACATGCCTAGGATTGTATTTAACTATCACCTATCTAA AAGAGGTATTCTCGCCTGCCTGGAAAGAATTTTGCTAAGAAAATTGTTTCTCTTCCC ATATTATTTTACCTCTATGCTAGTTCCCTGTGATTTGATATGTCAACTTTGACAAATTCA TTTTCTAAAGCACAGATATGACCTTTTTTGTTAAGAAAAAGAAACTACTGTTGCTCCCC 139738 GCTGTGGTTTGTTTTAATTCATCTCTAAGTATATTCTGATATCTCATGTGATTTCTCTT TTTGACTCTTTTTTTAAGAGTTTGTTGTTTAATTTCCACATTTTTGTGAATTTTCCAGTT TTCCTTCTGTTATTGATTCCTACCTTCATTCCAATTATTTCAGTCTTTTTAAATTTTTTG ATACCTGTTTTGTGGTTTCCTTCCATGGTTTCCTTTAACTCTGAGCATATTCAAGACGGT TGTTTTAAAATCTCACTCTAGAAAGCTCAATGTTTGAGCTTCCTCAGGACAATTTCTATC [T,C]GTTGATTTTAAGTCTTTGAATGGCAATATTTTCCTGTTTCTTTGTGTGCCTTGTGATTTT TTTTCTGTTGCTATTGAAAACTCGACATTTAAATATGATAATGTGGTAACTCTGGAAATC AGGTTCCTCCTTTCTTCATGGTTTGCTATTTTTTGATTGTTGAAGGCTGTAGTTATCCAT TGTTTAGCGACTTCTCCAAACAATGTTTGCAGAGATTGTCTGCTTTGTTGTCATCACT GAAGTTTCTGTTACTTTAGCCTGTGCTCAGCTAATGTTTTGACTGAGATTTAACACCAAG 140261 CTTTGTTGTCATCACTGAAGTTTCTGTTACTTTAGCCTGTGCTCAGCTAATGTTTTGA CTGAGATTTAACACCAAGAGCATTTTTAAGTTGTTTTTCTTTAATTTAGTGTTCAC TTGGTTCCAGTAAACCTTTGAGTGCTTTCCGGAGTTTTGACAAAGTTGGTTTTGACAGTA TCTGCTTGTTTTTTGATGTTTCTGTTCAGAGATGGGGCTTGGAACTGCTTACATCAGCA TTTTCTCTAGATTCTTCTAATCTTGTACCCCAGGTTCAAAAATAAAAGGTACTTTGCTT [C,T]AAAACAAAGAATAGTCTTTCTTCCAAGAAGAATCAGAAAGATTATGAACTATTTTTCTGA TTCTTCACTCTATTTTCTCTCTTTTACATTAAGGCTTTTAAAACATGAGTCAATCTTACC TTATTATATTAACATGCTCGTTCATTCATTCATTTATTCAGATGACTGTAAAA TTCCTGCTTTGTTAGGAAATATTTCTGACTAGGTGGTTAATGCTATGGTTAGATACACAA AGTGCTGTGGGAATTGCTCACTGGACCTGAGTGAAGGGTTAGGATAGGCTTTCCAGAGGA 141590 AATGGGAATAGCATTGAATCTATAAATTACTTTAGGCAGTATGGCCATTTTTATGATATT AGCAGTGGTTTGTATTTCTCCTTGAAGAGGTCCTTCATTTCCCTTGTTAGCTATATTCCT [T,G]

### FIGURE 3EEEE

GTTTCAGTATTTTAAAAACTTACTTCAGGTGATTCTATGTGTGCAACCATGATTGAGATA
CACTGTTATAGAATCTAGGATGTGATAAACTAGAAGAACATAACTAAAGTTTTGCATTTT
TCGGGTGTCTCAGTTTCCTCATTTATAGATGGAGTTGGTATGTGTACCAAGTTCATAGGC
TTGTTCTGAGTAAATTAGTGCATGTAAAGTGCTCCACAGAATGTTAGCTGTTGTGATGCT
TTACTTTCCATTGCACTTCCTGACTCCTAGCCTTTCTTTTCCTTGGCTCTTTTTATGCTC

142613 ACAAGTTGAACATGAACCCTTTAAGGGTAATGGGGTCTGAAGTGTCACACTAAAAGGTCA TCTGCAAGTATGTATTTCATATCTTTGTTTAAATAAAATAGTTACATAGTAGAGGGAAAA AAAATCCATGTGGATTTTGCATTTCACTCAATTATAACCTTGATTTTTAATGCTAAAAAT TATTTTCCTAAAATCTTGGGGTAAAAGTGTTGCTCCAAAGAGCTTTTATCAGATTATGT TTATCCTGTAGCTGCCTGTCCCCTGTGACCGATACTGGAAACCCTCAGGATTACAAATGC [C,T]TCCGTTTGCAAGTAAGAGTGAAATACAGCAGAACTGTGTCTTCTCCTTTGTCTTGTTCCC CATCTCTCTGTGCTTTGTATTGTTTCCTCTCTGTCACCTAAACAGGCACTCTGAAA TAAATGACTGAATGATTTTTTTAAAGAATATTTTCCATCAGAAGAAATTTGGAAGTATT TTGTTGCAGAATTTTAAAACATTTGATCTGGGTCTAATTCTGTCCTGGGACTGGTAATCA 142774 GATTTTTAATGCTAAAAATTATTTTTCCTAAAATCTTGGGGTAAAAGTGTTGCTCCAAAG AGCTTTTATCAGATTATGTTTATCCTGTAGCTGCCTGTCCCCTGTGACCGATACTGGAAA CCCTCAGGATTACAAATGCCTCCGTTTGCAAGTAAGAGTGAAATACAGCAGAACTGTGTC TTCTCCTTTGTCCCCCATCTCTTCTGTGCTTTGTATTGTTTCCTCTCTGTCA CCTAAACAGGCACTCTGAAAGAAAACTCTCCAGTACTGGAGAACTTAGCATATTCTAATT [C,A] GAAGAAATTTGGAAGTATTTTGTTGCAGAATTTTAAAACATTTGATCTGGGTCTAATTCT GTCCTGGGACTGGTAATCATCTTTTTTGAGGCTAAATTTTCTCATTTTGATGAAAAAGT CATCAATAGATGTTGAAAGCTGGACAGTGCAGTGTCAAAGCAAATGCTTTGCATGTCTGC AAGAAAGTCACAAATAAAGAAGGCTCTGCTGACTAAAAGAGAAAGATACTTAATCAACTC 143288 GTCAAAGCAAATGCTTTGCATGTCTGCAAGAAAGTCACAAATAAAGAAGGCTCTGCTGAC TAAAAGAGAAAGATACTTAATCAACTCCAGTACCATTGTTGAGGGGAACATTCTATCAGG ATTCAGTATAGAGAGATATTTTTAGGCTATTCACAAAATCCAGGTAGAACCTCCAAGCTA CATTTACAATAATACTAGCTTTTAGATTAATTGTTGTTTTTTAAATATGTATTAGCCTCT TATACAAATATAAGGAGTTACAAATTATTATTACAATAATCTTGGCTTTCGTGATTGTCC [G,A] ATGTATTTACACGTACCGAGAGCTTTATTTCTCCGTATAGTTTCAAGTTACTGTCTCGTG TCCTTTCATTTCACCTTGCAGGACTCCTTTGAGCATTTCTTACAGGGAAGTTCTAGTGGT AGTTCTGCCAGATAGAGGACCCTTGGTTGATAGGTTTTTTTCTTTTAGCACTTTGAATAT ATCAGCCCACTGCCTTCTGGCCTCCAAAGTTTCTGATAAGAAATCTGCCCGTCATCTTAT 145610 TCCCTCCCATGGGGCTGGAGGATGAGGGATGGGTAGCTGCTGCTGCTAAGAGCTTAAG TTGGTCATAATTAACTGCGCTTTGCCACCCAAGCCTTCCCTGAAAGTTGCAAGCTTTCAA TAGACTCCAGAGTTCTAAAATAGTGACATTAGACAGATTCTGCCAGTGCAATCGCTGTCT AGGAGGGGAGACAGATTCCTGGTGCTTCCTGTTTTGCCAGCTTCCCGGAATCTTCTTCAC TAGCATCCATTTTGAAGATACTACTTACTTCTCAATTTGGGGCTATTCATTGAATAGACT GTCACCAGGTTATTGGCTGTTTGAAGATTCTCATTTGTCTGCTAACTATACCTCTATTTT TTTTCTACGTTCACCTGGAAGACATGTCTTCTTCAAGAGCACCTTGACTCTGTCCAGAAG GAGTTCATAATTTTCAACAGAGAAAAGTAAGTAATTCCTGGGAGAACAACAGCCCCAGAA ATGGTGGCATGTTTCAGCCAGACTTTACTTGCAGAGAAAATATATTTTTAACATTTTAAA 148360 GAAGTGAACAGGCTTGGTGGGGGATTGTTTTCACCTCTTGGCTACTCAGAGTACCTAAAC CTGTCCTTACTTATGGAGAGCATGTGTCACACCAAGATGGCAGTAAGCTGGCAACTGCGA AGACCTGACTGATGCCCATTTGGGAAGCCAGGCAAGTGAAAATGGACCGAAGAAACAGAG ATGGCTGTCTTTTATGCAGGGCTTTTCCATAAAGAGGTTACACTGGGGCAACCAAGTATG TGTAGAAAGCCAGAGCTAAACTTCAGCTTGGCATTCACAGTTTTCTCTTCACTGAGCTAA [T,C]AGGCCCAGAGTTTCGGGCAGAGCTGTGAAATAGTGCTTCTCTAATAGCAACCATATTATT GTTACATAATTAAAAGCCAGCTCTTTTGTTTGTTTGATTCCTTTTTCCCTACAGTTCC

#### Chromosome map:

Chromosome 5

## FIGURE 3FFFF

CACATCATTTGTCTGTGTTTTTCTCCAAACACTATAAACTTGAAGCAATTGC

CCTGACTCGATTTCAGAGAAGGGGATG